

**STIC-Biotech/ChemLib**

174430

**From:** Dunston, Jennifer  
**Sent:** Friday, December 16, 2005 8:35 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence Search 10/659782

Please search the amino acid sequence of SEQ ID NO: 32 against the commercial nucleic acid databases.

Thank you.

Jennifer Dunston, Ph.D.  
USPTO Art Unit 1636  
REM 2B76  
Mailbox: REM 2C70  
(571) 272-2916

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\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up:  
Date completed: 12-16-05  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:36:08 ; Search time 164 Seconds

(without alignments)  
298.086 Million cell updates/sec

Title: US-10-659-782B-32  
Perfect score: 620

Sequence: 1 MPSPGTVCSLLLGMLWLDL.....PPSSRRRSRKSHQPSCSPEL 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417029326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/\_ptodata/1/pubpa/us07\_pubcomb.pep:  
2: /cgn2\_6/\_ptodata/1/pubpa/us08\_pubcomb.pep:  
3: /cgn2\_6/\_ptodata/1/pubpa/us09\_pubcomb.pep:  
4: /cgn2\_6/\_ptodata/1/pubpa/us10\_pubcomb.pep:  
5: /cgn2\_6/\_ptodata/1/pubpa/us10b\_pubcomb.pep:  
6: /cgn2\_6/\_ptodata/1/pubpa/us11\_pubcomb.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	605.5	97.7	116	5 US-10-659-782A-32	Sequence 32, App1	RESULT 2 US-10-294-191A-3
2	198	31.9	60	4 US-10-594-191A-3	Sequence 3, App1	Sequence 3, Application US-10294191A
3	198	31.9	91	4 US-10-477-506-2	Sequence 2, App1	Publication No. US20030211512A1
4	198	31.9	117	3 US-09-794-987-2	Sequence 2, App1	GENERAL INFORMATION:
5	198	31.9	117	3 US-09-553-253-2	Sequence 2, App1	APPLICANT: Rothschild, Max F.
6	198	31.9	117	3 US-09-389-722-268	Sequence 268, App	APPLICANT: Kim, Kwan Suk
7	198	31.9	117	3 US-09-389-723-268	Sequence 268, App	APPLICANT: Anderson, Lloyd L.
8	198	31.9	117	3 US-09-389-219-268	Sequence 268, App	APPLICANT: Novel Ghrelin Alleles and use of the Same for Genetically Typing I
9	198	31.9	117	3 US-09-389-721-268	Sequence 268, App	FILE REFERENCE: E05408US1
10	198	31.9	117	3 US-09-389-721-268	Sequence 268, App	CURRENT APPLICATION NUMBER: US/10/294, 191A
11	198	31.9	117	3 US-09-391-073-268	Sequence 268, App	CURRENT FILING DATE: 2002-11-14
12	198	31.9	117	3 US-09-391-442-268	Sequence 268, App	PRIOR APPLICATION NUMBER: US 60/333, 222
13	198	31.9	117	3 US-09-391-163-268	Sequence 268, App	PRIOR FILING DATE: 2001-11-14
14	198	31.9	117	3 US-09-393-604-268	Sequence 268, App	NUMBER OF SEQ ID NOS: 16
15	198	31.9	117	3 US-09-390-456-268	Sequence 268, App	SEQUENCE: 1
16	198	31.9	117	3 US-09-390-711-268	Sequence 268, App	SEQUENCE: 2
17	198	31.9	117	3 US-09-392-538-268	Sequence 268, App	SEQUENCE: 3
18	198	31.9	117	3 US-09-392-293A-268	Sequence 268, App	SEQUENCE: 4
19	198	31.9	117	3 US-09-393-744-268	Sequence 268, App	SEQUENCE: 5
20	198	31.9	117	3 US-09-393-744-268	Sequence 268, App	SEQUENCE: 6
21	198	31.9	117	3 US-09-391-181-268	Sequence 268, App	SEQUENCE: 7
22	198	31.9	117	3 US-09-391-181-268	Sequence 268, App	SEQUENCE: 8
23	198	31.9	117	3 US-09-390-730-268	Sequence 268, App	SEQUENCE: 9
24	198	31.9	117	3 US-09-390-446-268	Sequence 268, App	SEQUENCE: 10
25	198	31.9	117	3 US-09-393-687-268	Sequence 268, App	SEQUENCE: 11
26	198	31.9	117	3 US-09-398-714-268	Sequence 268, App	SEQUENCE: 12
27	198	31.9	117	3 US-09-397-653-268	Sequence 268, App	SEQUENCE: 13

#### ALIGNMENTS

RESULT 1  
US-10-659-782A-32

; Sequence 32, Application US/10659782A  
; Publication No. US20030059015A1  
; GENERAL INFORMATION:  
; APPLICANT: Mintz, Liat  
; TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing,  
; TREATING OBESITY AND/OR DIABETES

; FILE REFERENCE: 28238  
; CURRENT APPLICATION NUMBER: US/10/659, 782A  
; CURRENT FILING DATE: 2003-09-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 32  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-659-782A-32

Query Match Best Local Similarity 99.7%; Score 605.5; DB 5; Pred. No. 1.1e-57; Mismatches 0; Indel\_B 1; Gaps 1;

Qy 1 MPSPGTVCSLLGMWLDLAMAGSSFLSPEHQYQRPHKAPHIVPVLPLSNQCDLE 60  
Db 1 MPSPGTVCSLLGMWLDLAMAGSSFLSPEHQYQRPHKAPHIVPVLPLSNQCDLE 60  
Qy 61 QQRHMASVFSQSTKDSGSDLTVSSRTGAVLNPLFPPSSRERSRSRSHOPSCSPPL 117  
Db 61 QQRHMASVFSQSTKDSGSDLTVSSRTGAVLNPLFPPSSRERSRSRSHOPSCSPPL 116

RESUME

Sequence 3, Application US/10294191A  
; Publication No. US20030211512A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max F.  
; APPLICANT: Kim, Kwan Suk  
; APPLICANT: Anderson, Lloyd L.  
; FILE REFERENCE: E05408US1  
; CURRENT APPLICATION NUMBER: US/10/294, 191A  
; CURRENT FILING DATE: 2002-11-14  
; PRIORITY NUMBER: US 60/333, 222  
; PRIORITY FILING DATE: 2001-11-14  
; NUMBER OF SEQ ID NOS: 16  
; SEQUENCE: 1

PRIOR APPLICATION DATA:  
 TYPE: PRT APPLICATION NUMBER: 09/046,479  
 ORGANISM: Human  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sawislaw, Deborah A.  
 REGISTRATION NUMBER: 37,438  
 REFERENCE/DOCKET NUMBER: 97-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6672  
 TELEFAX: 206-442-6678  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-794-987-2

Query Match Score 198; DB 4; Length 60;  
 Best Local Similarity 88.4%; Pred. No. 9e-14; Indels 0; Gaps 0;  
 Matches 39; Conservative 0; Mismatches 5;

Y 1 MPSPGTVCSLLIGMMLDAMAGSSFLSPBHQVRPHKAP 44  
 b 1 MPSPGTVCSLLIGMMLDAMAGSSFLSPBHQVRQKESKKP 44

RESULT 3  
 Sequence 2, Application US/10477506  
 Publication No. US2004015722A1

GENERAL INFORMATION:  
 APPLICANT: Chopin, Leia K.  
 APPLICANT: Jeffery, Penelope L.  
 APPLICANT: Herrington, Adrian C.

TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY

FILE REFERENCE: 225181

CURRENT APPLICATION NUMBER: US/10/477,506  
 CURRENT FILING DATE: 2003-11-10  
 PRIOR APPLICATION NUMBER: PR9567  
 PRIOR FILING DATE: 2001-12-17  
 PRIOR APPLICATION NUMBER: PR4919  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: PCT/AU2/000582  
 PRIOR FILING DATE: 2002-05-10  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 2  
 LENGTH: 91

TYPE: PRT ORGANISM: Homo sapiens  
 S-10-477-506-2

Query Match Score 198; DB 4; Length 91;  
 Best Local Similarity 88.6%; Pred. No. 1.5e-13; Indels 0; Gaps 0;  
 Matches 39; Conservative 0; Mismatches 5;

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 b 1 MPSPGTVCSLLIGMMLDAMAGSSFLSPBHQVRQKESKKP 44

RESULT 4  
 Sequence 2, Application US/09794987  
 Patent No. US2001041791A1

GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 Designer, Theresa A.  
 TITLE OF INVENTION: MOTILIN HOMOLOGS  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 ZIP: 98102  
 COUNTRY: USA

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/794, 987  
 FILING DATE: 17-Feb-2001  
 CLASSIFICATION: <Unknown>

RESULT 5  
 Sequence 2, Application US/09853253  
 ; Sequence 2, Application US/09853253  
 ; Patent No. US2002005156A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaspers, STEPHEN  
 ; APPLICANT: SHEPPARD, PAUL  
 ; APPLICANT: DELSHER, THERESA  
 ; APPLICANT: BISHOP, PAUL  
 ; APPLICANT: FILE REFERENCE: 00-30  
 ; TITLE OF INVENTION: Zsg13-like Peptides  
 ; CURRENT APPLICATION NUMBER: US/09/853, 253  
 ; CURRENT FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: 60/203, 300  
 ; PRIOR FILING DATE: 2000-05-11  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PasteSEQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 117  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-853-253-2

Query Match Score 198; DB 3; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 2e-13; Indels 0; Gaps 0;  
 Matches 39; Conservative 0; Mismatches 5;

Qy 1 MPSPGTVCSLLIGMMLDAMAGSSFLSPBHQVRPHKAP 44  
 Db 1 MPSGTVCSSLIGMMLDAMAGSSFLSPBHQVRQKESKKP 44

RESULT 6  
 Sequence 268, App Application US/09989722  
 ; Sequence 268, App Application US/09989722  
 ; Patent No. US2002007206A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Borstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Borstein, David

/ APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerritsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Klavins, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Collin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / TITLE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: P273OP1C63  
 / CURRENT FILING DATE: 2001-11-19  
 / PRIOR APPLICATION NUMBER: 60/049787  
 / PRIOR FILING DATE: 1997-06-16  
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; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match Score 198; DB 3; Length 117;  
Best Local Similarity 88.6%; Pred. No. 2e-13; Mismatches 5; Indels 0; Gaps 0;  
Matches 39; Conservative 0;

Qy 1 MPSPGTVCSLLGMLWLDAMAGSSFLSSEHQRVQVRPHKAP 44  
Db 1 MPSPGTVCSLLGMLWLDAMAGSSFLSSEHQRVQQRKESKKP 44

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RESULT 7  
US-09-989-723-268  
Sequence 268, Application US/09989723  
Patent No. US2002007202A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyer, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hans Peter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Hwang, William I.  
APPLICANT: Kjavian, Ivar J.  
APPLICANT: Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2230P1C62  
CURRENT APPLICATION NUMBER: US/09/989 , 723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-24  
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

Query Match          31.9% ; Score 198; DB 3; Length 117;
Best Local Similarity 88.6% ; Pred. No. 2e-13; Matches 39; Gaps 0;
Matches 39; Conservatve 0; Mismatches 5; Indels 8 ; Db 1 MPSPTVCSULLGMWLAMAGSSFLSBEHQVRPHKAP 44
Qy 1 MPSPTVCSULLGMWLAMAGSSFLSBEHQVRQKESKKP 44
Db 1 MPSPTVCSULLGMWLAMAGSSFLSBEHQVRQKESKKP 44

RESULT 8
US-0-989-279-268
Sequence 268, Application US/09989279
; Parent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hansperter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napiir, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: 
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zarin, Zemini
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILING NUMBER: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 31.9%; Score 198; DB 3; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 2e-13; Mismatches 0; Gaps 0;

Qy	1	MPSPGTVCSLLLGMMWLDAMAGSSFLSPHEHQVRQVRPHKAP 44
Db	1	MPSPGTVCSLLLGMMWLDAMAGSSFLSPHEHQVRQQRKESKKP 44

RESULT 9  
 US-09-989-727-268  
 Sequence 268, Application US/09989727  
 Patent No. US20020072497A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William J.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          Score 198; DB 3;
Best Local Similarity 88.6%; Pred. No. 2e-13;
Matches 39; Conservative 0; Mismatches 5; Indel 8
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Db      1 MPSPTGTVCSLLLGMWLDLAMAGSSFLSPHQYVQRKESKKP 44

RESULT 10
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Sequence 268, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi J.
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan L.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gerber, Hanspeter
;   APPLICANT: Gerritsen, Mary E.
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, J. Christopher
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Klijavins, Ivar J.
;   APPLICANT: Napier, Mary A.
;   APPLICANT: Pan, James
;   APPLICANT: Paon, Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Tumaa, Daniel
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William T.
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P273051C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/092250
; PRIOR FILING DATE: 1997-10-16

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; PRIOR APPLICATION NUMBER: 60/091360  
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 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match      Score 198;    DB 3;    Length 117;  
 Best Local Similarity 88.6%;    Pred. No. 2e-13;    Indels 0;    Gaps 0;

Qy	1	MPSPGTVCSLLGMLWLDAMAGGSFLSDEHQVRQVRPHKAP 44
Db	1	MPSPGTVCSLLGMLWLDAMAGGSFLSDEHQVRQQRKESKKP 44

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RESULT 11  
 US-09-989-732-268  
 Sequence 268, Application US/09989732  
 Patent No. US20020123463A1

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi J.
- APPLICANT: Baker, Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Eaton, Dan L.
- APPLICANT: Ferrara, Napoleone
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Klijavins, Ivar J.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tumas, Daniel
- APPLICANT: Watanabe, Colin K.
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William I.
- APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic acids Encoding the Same

CURRENT APPLICATION NUMBER: US/09/989,732  
 FILE REFERENCE: P2730PIC57

PRIOR APPLICATION NUMBER: 60/04787  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLILGMWLDLAMAGSSFLSPHEHQVRPPHKAP 44
Db 1 MPSPGTVCSSLILGMWLDLAMAGSSFLSPHEHQVRQRKESKKP 44

RESULT 12
US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavinc, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watarabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS Encoding the Same
; FILE REFERENCE: F2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
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 Best Local Similarity      88.6%;    Pred. No. 2e-13;  
 Matches      39;    Conservative 0;    Mismatches 5;    Indels 0;    Gaps 0;  
  
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 Db      1. MPSPGTVCSLLGMLWDLAMAGSSFLSPEHQRVQQRKSKKP 44

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RESULT 13

US-09-990-442-268

Sequence 268, Application US/0990442  
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 GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Klijavín, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2230PBCB  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

	Matches	39;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
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Db	1	MPSPGTVCSLLLGMLWLDLAMAGSSFLSPEHQVRQPRKESKKP	44							

RESULT 14  
 US-09-991-163-268  
 Sequence 268, Application US/09991163  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Borstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavini, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tuman, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William J.  
 ; APPLICANT: Zemlin, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; ACIDS Encoding the Same  
 ; FILE REFERENCE: P2730P1C17  
 ; CURRENT APPLICATION NUMBER: US/09/991,163  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
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Query Match Similarity 31.9%; Score 198; DB 3; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 2e-13;

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; PRIOR APPLICATION NUMBER: 60/089307 ; PRIOR FILING DATE: 1998-07-02
; PRIOR FILING DATE: 1998-06-18 ; Query Match Score 198: DB 3; Length 117;
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; PRIOR FILING DATE: 1998-06-19 ; PRIOR APPLICATION NUMBER: 60/090246

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RESULT 15
US-09-993-604-268
Sequence 268, Application US/09993604
Patent No. US2002013705A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Destroyer, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C25

CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23

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Page 17

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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match Score 198; DB 3; Length 117;  
Best Local Similarity 88.6%; Pred. No. 2e-13;  
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSPGTVCSLLIGMLDLMAGSSPLSPERQVRPDKAP 44  
Db 1 MSPGTVCSLLIGMLDLMAGSSPLSPERQVRQKESKKP 44

L S P E H Q R V Q V 37

Search completed: December 21, 2005, 13:44:36  
Job time : 166 secs

*This Page Blank (uspto)*

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:25:12 ; Search time 187 Seconds

(without alignments)

274.905 Million cell updates/sec

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1: geneseqP1980s:\*

2: geneseqP1980s:\*

3: geneseqP2001s:\*

4: geneseqP2001s:\*

5: geneseqP2002s:\*

6: geneseqP2003as:\*

7: geneseqP2003bs:\*

8: geneseqP2004s:\*

9: geneseqP2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	605.5	97.7	116 9 ADY78074	Ady78074 Human ghr
2	198	31.9	60 8 ADK66754	Adk66754 Human ghr
3	198	31.9	91 6 AAE33410	Aae33410 Human exo
4	198	31.9	117 2 AAW87991	Aaw87991 Protein d
5	198	31.9	117 3 AAY87236	Aay87236 Human sig
6	198	31.9	117 4 AAB20101	Aab20101 Zsig33 pr
7	198	31.9	117 4 AAB62649	Aab62649 Human zsi
8	198	31.9	117 4 AAM38890	Aam38890 Human pol
9	198	31.9	117 4 AAB60511	Aab60511 Human ghr
10	198	31.9	117 5 ABB78319	Abb78319 Amino aci
11	198	31.9	117 5 AAB23838	Aae23838 Human zsi
12	198	31.9	117 5 AAE15883	Aae15883 Human zsi
13	198	31.9	117 6 ABUS046	Abus046 Human PRO
14	198	31.9	117 6 ABUS9124	Abus9124 Novel hum
15	198	31.9	117 6 ABU82636	Abu82636 Human sec
16	198	31.9	117 6 ABO1733	Abol1733 Novel hum
17	198	31.9	117 6 ABU60555	Abu60555 Human sec
18	198	31.9	117 6 ABU13937	Abu13937 Human PRO
19	198	31.9	117 6 ABU81090	Abu81090 Human PRO
20	198	31.9	117 6 ABU72522	Abu72522 Novel hum
21	198	31.9	117 6 ABU66790	Abu66790 Human PRO
22	198	31.9	117 6 ABUS9871	Abus9871 Novel sec
23	198	31.9	117 6 ABUS9271	Abus9271 Human sec
24	198	31.9	117 6 ABO25968	Abo25968 Human PRO

#### ALIGNMENTS

#### RESULT 1

ADY78074

ADY78074 standard; protein; 116 AA.

XX

AC

XX

DT

02-JUN-2005 (first entry)

XX

Human ghrelin variant 2 protein, SEQ ID NO: 32.

DE

XX

Diagnosis; obesity; anorectic; nutritional disorder; diabetes;

KW

antidiabetic; endocrine disease; metabolic disorder;

KW

gastrointestinal disease; drug screening; gene therapy; ghrelin.

XX

Homo sapiens.

OS

XX

FH

Misc-difference 64.

65

/note= "Encoded by CATCTCTGG"

Location/Qualifiers

Key

FT

PT

XX

US2005059015-A1.

XX

XX

PD

17-MAR-2005.

XX

PP

11-SEP-2003; 2003US-00655782.

XX

PR

11-SEP-2003; 2003US-00655782.

XX

PA

(MINTZ L.

XX

PI

Mintz L.

XX

XX

WPI; 2005-240894/25.

DR

N-PSDB; ADY7803.

XX

CC

The invention relates to alternative splice variants of the obesity

and/or diabetes related genes and their corresponding proteins. The

invention also relates to compositions, reagents, kits and methods for

diagnosing, monitoring and treating obesity and/or diabetes. The

composition and methods are useful for diagnosing, monitoring and

treating obesity and/or diabetes. These may also be used in drug

screening purposes.

XX

Claim 32; SEQ ID NO 32; 74pp; English.

CC screening purposes and in gene therapy. The present sequence is the human  
 CC ghrelin (GHRL) variant protein. This protein is encoded by an obesity and  
 CC diabetes related gene.  
 XX Sequence 116 AA;

Query Match 97.7%; Score 605.5; DB 9; Length 116;  
 Best Local Similarity 99.1%; Pred. No. 8.3e-61;  
 Matches 116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 Qy ADK66754 standard; protein; 60 AA.

RESULT 3  
 ID AAE33410  
 ID AAE33410 Standard; protein; 91 AA.  
 XX  
 AC AAE33410;  
 DT 02-APR-2003 (first entry)  
 XX  
 DE Human exon 3-deleted ghrelin protein.  
 XX  
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;  
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;  
 KW cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200290387-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 10-MAY-2002; 2002WO-AU000582.  
 XX  
 PR 10-MAY-2001; 2001AU-00004919.  
 PR 17-DEC-2001; 2001AU-00009567.  
 XX  
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
 XX  
 PI Chopin LK, Jeffery PL, Herington AC;  
 XX  
 DR WPI; 2003-111957/10.  
 DR N-PSDB; AAD50726.

© Human ghrelin protein #1.  
 XX  
 Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;  
 XX breeding; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003211512-A1.  
 XX  
 PD 13-NOV-2003.  
 XX  
 PF 14-NOV-2002; 2002US-00294191.  
 XX  
 PR 14-NOV-2001; 2001US-0333222P.  
 XX  
 PA (ROTH/) ROTHSCHILD M F.  
 PA (KIMK/) KIM K.  
 PA (ANDE/) ANDERSON L L.  
 XX  
 PI Rothchild MF, Kim K, Anderson LL;  
 XX  
 DR 2004-010667/01.  
 XX  
 PT Screening animals (i.e. pigs) to determine those more likely to produce  
 desired growth, appetite and fatness to optimize breeding and selection  
 PT techniques comprises detecting the presence of a polymorphism in the  
 PT Ghrelin gene.  
 XX  
 Disclosure: SEQ ID NO 3; 24pp; English.  
 XX  
 The present invention relates to a method of screening animals to  
 CC determine those more likely to produce desired growth, appetite and  
 CC fatness which involves obtaining a sample of genetic material from the  
 CC animal and assaying for the presence of a genotype in the animal which is  
 CC associated with favourable growth, appetite and fatness, the genotype  
 CC characterised by a polymorphism in the ghrelin gene. The composition and  
 CC methods are useful in screening animals (i.e. pigs) to determine those  
 CC more or less likely to produce desired growth, appetite and fatness to  
 CC optimise breeding and selection techniques. The present sequence is human  
 CC ghrelin protein of the invention.  
 XX Sequence 60 AA;

Query Match 31.9%; Score 198; DB 8; Length 60;  
 Best Local Similarity 88.6%; Pred. No. 1.2e-14;  
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 4  
 ID AAW87991  
 XX  
 AC AAW87991;  
 XX  
 ID AAW87991 Standard; protein; 117 AA.  
 XX  
 DR 07-APR-1999 (first entry)

DE Protein designated zsig33.  
 XX 2sig33; gastric motility; gastrointestinal inflammation; reflux disease;  
 KW nutrient absorption regulation; obesity; metabolic disorder.

## Homo sapiens.

XX Key Peptide Location/Qualifiers  
 FT 1..23 /note= "signal peptide"  
 FT 24..117 /note= "mature protein"  
 XX WO9842840-A1.

PD 01-OCT-1998. XX PF 23-MAR-1998; 98W0-US005620.  
 PR 24-MAR-1997; 97US-0041102P.  
 PR 24-MAR-1997; 97US-0082897.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX Sheppard PO, Deisher TA;  
 PI DR: 1999-070071/06.  
 DR N-PSDB; AAX04550.

XX Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility.  
 XX Claim 13; Page 55-56; 69pp; English.  
 PS The present sequence represents a protein designated zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate Gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes/ acids, gastrointestinal motility, recruitment of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient absorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33 agonists, antagonists and ligands and to produce antibodies.

XX Sequence: 117 AA;

CC Query Match 31.9%; Score 198; DB 2; Length 117;  
 CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;  
 CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 3; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 4; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 5; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 6; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 7; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 8; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 9; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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CC Query Match 31.9%; Score 198; DB 10; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 12; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 13; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 14; Length 117;

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CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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CC Query Match 31.9%; Score 198; DB 19; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 20; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 21; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 22; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 23; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 24; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 25; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 26; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 27; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 28; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 29; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 30; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 31; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 32; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 33; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 34; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 35; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 36; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 37; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 38; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 39; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 40; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 41; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 42; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 43; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 44; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 45; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 46; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 47; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 48; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 49; Length 117;

CC Best Local Similarity 88.6%; Pred. No. 2.8e-14;

CC Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC Sq Sequence 117 AA;

CC Query Match 31.9%; Score 198; DB 50; Length 117;

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XX	ABB78319;	KW Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
AC	05-DBC-2002 (first entry)	
XX	D	
XX	Amino acid sequence of a human zsig33.	
XX	Short gastrointestinal peptide; SGIP; zsig33; motilin.	
XX	OS Homo sapiens.	
XX	Key Location/Qualifiers	
FH	1 .23	
FT Peptide	/note= "signal peptide"	
FT Protein	24 .119	
FT	/note= "mature protein"	
XX	US6420521-B1.	
XX	PD 16-JUL-2002.	
XX	PP 30-JUN-2000; 2000US00608810.	
XX	PR 30-JUN-1999; 99US0141592P.	
XX	(ZYMO ) ZYMOGENETICS INC.	
PA	P1 Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;	
PS	PS Disclosure; Col 39-40; 23pp; English.	
XX	DR WPI; 2002-634794/68.	
DR	N-PSPDB; ABV72214.	
XX	New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders.	
PT		
XX	The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP. SGIP may also be used as an antigen in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antagonists may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used as diagnostic agents for detecting the presence of SGIP in samples.	
XX	SQ Sequence 117 AA;	
XX	Query Match Score 198; DB 5; Length 117;	
	Best Local Similarity 88.8%; Pred. No. 2.8e-14;	
	Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Qy	1 MPSPGTVCSLLGLMNLWLDLAMAGSSFLSPHEHQVRVQVRPHKAP 44	
Db	1 MPSPGTVCSLLGLMNLWLDLAMAGSSFLSPHEHQVRVQQRKESKKP 44	
RESULT 11		
AAE23838	ID AAE15883 standard; protein; 117 AA.	
ID	XX	
AAE23838	AC AAE15883;	
XX	XX	
AC	XX	
AAE23838;	DT 26-MAR-2002 (first entry)	
XX	DE Human zsig33 protein.	
DE	XX	
Human zsig33 protein.	KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;	
XX	XX	
XX	XX	
XX	OS Homo sapiens.	
XX	PN US200205156-A1.	
XX	PD 09-MAY-2002.	
XX	PP 10-MAY-2001; 2001US00853253.	
XX	PR 11-MAY-2000; 2000US0203300P.	
XX	PA (JASPER/) JASPER S. R.	
PA	(SHEP/) SHEPPARD P.O.	
PA	(DEIS/) DEISHER T.A.	
PA	(BISH/) BISHOP P.D.	
XX	PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;	
XX	PS Disclosure; Page 27; 34pp; English.	
XX	DR WPI; 2002-442750/47.	
DR	N-PSDB; AAD38238.	
XX	ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones.	
PT		
XX	CC The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression.	
CC	CC The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. Zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein.	
XX	SQ Sequence 117 AA;	
XX	Query Match Score 198; DB 5; Length 117;	
	Best Local Similarity 88.6%; Pred. No. 2.8e-14;	
	Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Qy	1 MPSPGTVCSLLGLMNLWLDLAMAGSSFLSPHEHQVRVQVRPHKAP 44	
Db	1 MPSPGTVCSLLGLMNLWLDLAMAGSSFLSPHEHQVRVQQRKESKKP 44	
RESULT 12		
AAE15883	ID AAE15883 standard; protein; 117 AA.	
ID	XX	
AAE15883;	AC AAE15883;	
XX	XX	
AC	XX	
AAE15883;	DT 26-MAR-2002 (first entry)	
XX	DE Human zsig33 protein.	
DE	XX	
Human zsig33 protein.	KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;	
XX	XX	

KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;  
 KW absorption enhancer; gastrointestinal disease; growth related disease;  
 KW inflammation; gene therapy; growth regulation; blood vessel formation;  
 KW HIV; zsig33 protein.

XX OS Homo sapiens.

XX Key Peptide 1..23  
 FT FT Location/Qualifiers /label= Signal\_peptide  
 FT Protein 24 ..117 /note= "Human mature zsig33 protein"

XX PN WO200187933-A2.

XX PD 22-NOV-2001.

XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-082982/11.

XX DR N-PSDB; ADD25759.

XX PT New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like peptides.

XX Disclosure; Page 80-81; 89pp; English.

XX The invention relates to zsig33-like peptides (ZS33LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon peptides and nucleic acid molecules encoding such zsig33-like peptides. ZS33LP peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other development processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as absorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. ZS33LP peptides, nucleic acids and/or antibodies are useful for treating disorders associated with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33 protein.

XX Sequence 117 AA;

Query Match 31.9%; Score 198; DB 5; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 2..8e-14;  
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLGMLWDLAMAGSSFLSPERHQVTRPMPHAK 44  
 Db 1 MPSPGTVCSLLLGMLWDLAMAGSSFLSPERHQVTRPMPHAK 44

RESULT 13  
 ABUS8046 standard; protein; 117 AA.  
 ID ABUS8046;  
 XX AC ABUS8046;  
 DT 14-APR-2003 (first entry)  
 DE Human PRO polypeptide #78.  
 XX Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;  
 KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX OS Homo sapiens.  
 XX PN US2003027163-A1.  
 XX PD 06-FEB-2003.  
 XX PF 15-NOV-2001; 2001US-00997666.  
 PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0067250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0065116P.  
 PR 13-NOV-1997; 97US-0065111P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088125P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 04-JUN-1998; 98US-0088328P.  
 PR 04-JUN-1998; 98US-0088329P.  
 PR 04-JUN-1998; 98US-0088330P.  
 PR 04-JUN-1998; 98US-0088333P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088302P.  
 PR 05-JUN-1998; 98US-0088312P.  
 PR 05-JUN-1998; 98US-0088317P.  
 PR 09-JUN-1998; 98US-008855P.  
 PR 10-JUN-1998; 98US-0088334P.  
 PR 10-JUN-1998; 98US-0088338P.  
 PR 10-JUN-1998; 98US-0088342P.  
 PR 10-JUN-1998; 98US-0088310P.  
 PR 10-JUN-1998; 98US-0088324P.  
 PR 10-JUN-1998; 98US-0088326P.  
 PR 11-JUN-1998; 98US-0088314P.  
 PR 11-JUN-1998; 98US-0088332P.  
 PR 11-JUN-1998; 98US-0088338P.  
 PR 11-JUN-1998; 98US-0088342P.  
 PR 11-JUN-1998; 98US-0088376P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089140P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089332P.  
 PR 17-JUN-1998; 98US-0089338P.  
 PR 17-JUN-1998; 98US-008998P.  
 PR 17-JUN-1998; 98US-008999P.  
 PR 17-JUN-1998; 98US-008900P.  
 PR 17-JUN-1998; 98US-008953P.  
 PR 18-JUN-1998; 98US-008901P.  
 PR 18-JUN-1998; 98US-008907P.  
 PR 18-JUN-1998; 98US-008908P.

PR 19-JUN-1998; 98US-0089947P.  
 PR 19-JUN-1998; 98US-0089948P.  
 PR 19-JUN-1998; 98US-0089952P.  
 PR 22-JUN-1998; 98US-009046P.  
 PR 22-JUN-1998; 98US-009052P.  
 PR 22-JUN-1998; 98US-0090254P.  
 PR 23-JUN-1998; 98US-0090349P.  
 PR 23-JUN-1998; 98US-0090355P.  
 PR 24-JUN-1998; 98US-0090429P.  
 PR 24-JUN-1998; 98US-0090431P.  
 PR 24-JUN-1998; 98US-0090435P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 24-JUN-1998; 98US-0090445P.  
 PR 25-JUN-1998; 98US-0090472P.  
 PR 25-JUN-1998; 98US-0090525P.  
 PR 25-JUN-1998; 98US-0090535P.  
 PR 25-JUN-1998; 98US-0090540P.  
 PR 25-JUN-1998; 98US-0090542P.  
 PR 25-JUN-1998; 98US-0090557P.  
 PR 26-JUN-1998; 98US-0090676P.  
 PR 26-JUN-1998; 98US-0090678P.  
 PR 26-JUN-1998; 98US-0090690P.  
 PR 26-JUN-1998; 98US-0090694P.  
 PR 26-JUN-1998; 98US-0090695P.  
 PR 26-JUN-1998; 98US-0090696P.  
 PR 01-JUL-1998; 98US-0091160P.  
 PR 01-JUL-1998; 98US-0091164P.  
 PR 02-JUL-1998; 98US-0091178P.  
 PR 02-JUL-1998; 98US-0091191P.  
 PR 02-JUL-1998; 98US-0091162P.  
 PR 02-JUL-1998; 98US-0091163P.  
 PR 02-JUL-1998; 98US-0091160P.  
 PR 02-JUL-1998; 98US-0091164P.  
 PR 02-JUL-1998; 98US-0091173P.  
 PR 07-JUL-1998; 98US-00911978P.  
 PR 07-JUL-1998; 98US-00911982P.  
 PR 09-JUL-1998; 98US-00911628P.  
 PR 02-JUL-1998; 98US-00911633P.  
 PR 02-JUL-1998; 98US-00911646P.  
 PR 30-JUL-1998; 98US-0091173P.  
 PR 04-AUG-1998; 98US-00911978P.  
 PR 04-AUG-1998; 98US-0095282P.  
 PR 10-AUG-1998; 98US-0095285P.  
 PR 04-AUG-1998; 98US-0095301P.  
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 PR 04-AUG-1998; 98US-0095318P.  
 PR 04-AUG-1998; 98US-0095321P.  
 PR 04-AUG-1998; 98US-0095325P.  
 PR 10-AUG-1998; 98US-0095316P.  
 PR 17-AUG-1998; 98US-0095329P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 17-AUG-1998; 98US-0096716P.  
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 PR 17-AUG-1998; 98US-0096894P.  
 PR 17-AUG-1998; 98US-0096012P.  
 PR 11-AUG-1998; 98US-0096143P.  
 PR 12-AUG-1998; 98US-0096512P.  
 PR 17-AUG-1998; 98US-0096757P.  
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 PR 18-AUG-1998; 98US-0097022P.  
 PR 18-AUG-1998; 98US-0097141P.  
 PR 19-AUG-1998; 98US-009718P.  
 PR 24-AUG-1998; 98US-0097561P.  
 PR 26-AUG-1998; 98US-009752P.

PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097955P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097974P.  
 PR 26-AUG-1998; 98US-0097978P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 26-AUG-1998; 98US-0097986P.  
 PR 26-AUG-1998; 98US-0098014P.  
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 PR 16-SEP-1998; 98US-0100634P.  
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 PR 17-SEP-1998; 98US-0100858P.  
 PR 17-SEP-1998; 98US-019437P.  
 PR 07-OCT-1998; 98US-0192141P.  
 PR 01-DEC-1998; 98US-0192125P.  
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 PR 08-MAR-1999; 99US-00905028P.  
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 PR 02-JUN-1999; 99US-0141037P.  
 PR 23-JUN-1999; 99US-0141037P.  
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 PR 17-AUG-1999; 99US-0149396P.  
 PR 02-SEP-1999; 99US-0152109P.  
 PR 15-SEP-1999; 99US-01521547P.  
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 PR 30-NOV-1999; 99US-015828313P.  
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 PR 17-DEC-1999; 99US-014928301P.  
 PR 16-DEC-1999; 99US-014928301P.  
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 PR 06-JAN-2000; 200000-0-US00376P.  
 PR 11-FEB-2000; 200000-0-US003565P.  
 PR 18-FEB-2000; 200000-0-US004341P.  
 PR 22-FEB-2000; 200000-0-US004414P.  
 PR 20-MAR-2000; 200000-0-US007377P.  
 PR 24-FEB-2000; 200000-0-US0104914P.  
 PR 05-MAR-2000; 200000-0-US005004P.  
 PR 06-MAR-2000; 200000-0-US013358P.  
 PR 12-MAR-2000; 200000-0-US013705P.  
 PR 10-MAR-2000; 200000-0-US014042P.  
 PR 15-MAR-2000; 200000-0-US013119P.  
 PR 20-MAR-2000; 200000-0-US007684P.  
 PR 30-MAR-2000; 200000-0-US015264P.  
 PR 23-TUN-2000; 200000-0-US01337P.  
 PR 15-MAY-2000; 200000-0-US013358P.  
 PR 17-MAY-2000; 200000-0-US013705P.  
 PR 22-MAY-2000; 200000-0-US014042P.  
 PR 30-MAY-2000; 200000-0-US013119P.  
 PR 02-JUN-2000; 200000-0-US015264P.  
 PR 23-JUN-2000; 200000-0-US01337P.  
 PR 28-JUL-2000; 200000-0-US020710P.  
 PR 11-AUG-2000; 200000-0-US022031P.  
 PR 23-AUG-2000; 200000-0-US023522P.  
 PR 24-AUG-2000; 200000-0-US023328P.  
 PR 07-SEP-2000; 200000-0-US020978P.

Query Match 31.9%; Score 199;  
 Best Local Similarity 88.6%; DB 6;  
 Matches 39; Length 117;  
 Conservative 0; Pred. No. 2.8e-14;  
 Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLQLGMWLDAAGSSFLSPEHQVRPHKAP 44  
 Db 1 MPSPTVCSLLLQLGMWLDAAGSSFLSPEHQVRQKRKESKKP 44

RESULT 14  
 ABUS9124  
 ID ABUS9124 standard; protein; 117 AA.  
 XX  
 AC ABUS9124;  
 XX



useful for treating cancerous tumours. PROB12 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PROB26, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune responses. PROB28, PRO26, PRO1058 or PRO132 enhance survival of retinal neurons cells (PRO112 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD, PROB19, PROB13 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO841, PRO112, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein

XX Sequence 117 AA;

Query Match Similarity 31.3%; Score 198; DB 6; Length 117;  
Best Local Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MPSPGIVCSLLLGMWLDAAGSSFLSPEHQVRVQRPHKAP 44  
Db 1 MPSPGIVCSLLLGMWLDAAGSSFLSPEHQVRVQRKESKKP 44

**RESULT 15**  
ID ABU82636 Standard; protein, 117 AA.

XX ABU82636;

XX DT 26-JUN-2003 (first entry)

**DE Human secreted/transmembrane protein PRO1066.**

XX Human; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2003032023-A1.

XX 13-FEB-2003.

XX 14-NOV-2001; 2001US-00990711.

XX PR 16-JUN-1997; 97US-0049787P.

PR 05-NOV-1997; 97US-0062250P.

PR 17-OCT-1997; 97US-002006.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 03-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

CC	useful for treating cancerous tumours. PROB12 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PROB26, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune responses. PROB28, PRO26, PRO1058 or PRO132 enhance survival/proliferation of retinal neurons cells (PRO112 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD, PROB19, PROB13 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO841, PRO112, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein	XX	Sequence 117 AA;	PR	04-JUN-1998; 98US-0088028P.
CC			PR	04-JUN-1998; 98US-0088029P.	
CC			PR	04-JUN-1998; 98US-0088030P.	
CC			PR	04-JUN-1998; 98US-0088033P.	
CC			PR	04-JUN-1998; 98US-0088326P.	
CC			PR	05-JUN-1998; 98US-0088167P.	
CC			PR	05-JUN-1998; 98US-0088202P.	
CC			PR	05-JUN-1998; 98US-0088212P.	
CC			PR	05-JUN-1998; 98US-0088217P.	
CC			PR	09-JUN-1998; 98US-0088655P.	
CC			PR	10-JUN-1998; 98US-0088734P.	
CC			PR	10-JUN-1998; 98US-0088738P.	
CC			PR	10-JUN-1998; 98US-0088742P.	
CC			PR	10-JUN-1998; 98US-0088810P.	
CC			PR	10-JUN-1998; 98US-0088824P.	
CC			PR	11-JUN-1998; 98US-0088826P.	
CC			PR	11-JUN-1998; 98US-0088861P.	
CC			PR	11-JUN-1998; 98US-0088876P.	
XX			PR	12-JUN-1998; 98US-0089105P.	
SQ			PR	16-JUN-1998; 98US-0089440P.	
			PR	16-JUN-1998; 98US-0089512P.	
			PR	16-JUN-1998; 98US-0089514P.	
			PR	17-JUN-1998; 98US-0089532P.	
			PR	17-JUN-1998; 98US-0089538P.	
			PR	17-JUN-1998; 98US-0089598P.	
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			PR	17-JUN-1998; 98US-0089600P.	
			PR	18-JUN-1998; 98US-0089801P.	
			PR	18-JUN-1998; 98US-0089907P.	
			PR	19-JUN-1998; 98US-0089947P.	
			PR	19-JUN-1998; 98US-0089948P.	
			PR	19-JUN-1998; 98US-0089952P.	
			PR	22-JUN-1998; 98US-0090246P.	
			PR	22-JUN-1998; 98US-0090252P.	
			PR	22-JUN-1998; 98US-0090254P.	
			PR	23-JUN-1998; 98US-0090349P.	
			PR	23-JUN-1998; 98US-0090355P.	
			PR	24-JUN-1998; 98US-0090429P.	
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			PR	24-JUN-1998; 98US-0090472P.	
			PR	24-JUN-1998; 98US-0090540P.	
			PR	24-JUN-1998; 98US-0090542P.	
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			PR	25-JUN-1998; 98US-0090676P.	
			PR	25-JUN-1998; 98US-0090678P.	
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			PR	25-JUN-1998; 98US-0090694P.	
			PR	25-JUN-1998; 98US-0090695P.	
			PR	26-JUN-1998; 98US-0090696P.	
			PR	26-JUN-1998; 98US-0090697P.	
			PR	01-JUL-1998; 98US-0091360P.	
			PR	02-JUL-1998; 98US-0091478P.	
			PR	02-JUL-1998; 98US-0091673P.	
			PR	07-JUL-1998; 98US-0091978P.	
			PR	07-JUL-1998; 98US-0091982P.	
			PR	09-JUL-1998; 98US-0092182P.	
			PR	10-JUL-1998; 98US-0092472P.	
			PR	20-JUL-1998; 98US-009339P.	
			PR	30-JUL-1998; 98US-0094651P.	

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	Query Match	Best Local Similarity	Score	DB 6;	Length
	Matches	Conservative	88.6%;	Pred. No. 2	117;
			0; Mismatches	Indels	0; Gaps
Qy	1	MPSPGTVCSLLIIGMLWLAMAGSSFLSPEHQVQRPHKAP 44			
Db	1	MPSGTGVCSLLIIGMLWLAMAGSSFLSPEHQVQRKESKKP 44			

Search completed: December 21, 2005, 13:36:00  
Job time : 190 secs

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PR 04-AUG-1998; 98US-0095282P;  
PR 04-AUG-1998; 98US-0095285P;  
PR 04-AUG-1998; 98US-0095301P;  
PR 04-AUG-1998; 98US-0095302P;  
PR 04-AUG-1998; 98US-0095311P;  
PR 04-AUG-1998; 98US-0095318P;  
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PR 04-AUG-1998; 98US-0095325P;  
PR 10-AUG-1998; 98US-0095916P;  
PR 10-AUG-1998; 98US-0095929P;  
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PR 17-AUG-1998; 98US-0096757P;  
PR 17-AUG-1998; 98US-0096766P;  
PR 17-AUG-1998; 98US-0096768P;  
PR 17-AUG-1998; 98US-0096773P;  
PR 17-AUG-1998; 98US-0096791P;  
PR 17-AUG-1998; 98US-0096867P;  
PR 17-AUG-1998; 98US-0096919P;  
PR 17-AUG-1998; 98US-0096949P;  
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PR 19-AUG-1998; 98US-0097141P;  
PR 20-AUG-1998; 98US-0097218P;  
PR 24-AUG-1998; 98US-0097561P;  
PR 26-AUG-1998; 98US-0097952P;  
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PR 26-AUG-1998; 98US-0097971P;  
PR 26-AUG-1998; 98US-0097974P;  
PR 26-AUG-1998; 98US-0097978P;  
PR 26-AUG-1998; 98US-0097979P;  
PR 26-AUG-1998; 98US-0097986P;  
PR 26-AUG-1998; 98US-0098014P;  
PR 31-AUG-1998; 98US-009825P;  
PR 16-SEP-1998; 98US-0100634P;  
PR 16-SEP-1998; 98WO-US019330;  
PR 17-SEP-1998; 98US-0100858P;  
PR 17-SEP-1998; 98WO-US019437;  
PR 07-OCT-1998; 98WO-US021141;  
PR 02-JUN-1999; 98WO-US02108P;  
PR 02-JUN-1999; 98US-0113296P;  
PR 05-DAN-1999; 99WO-US0001;  
PR 08-MAR-1999; 99WO-US005028;  
PR 12-MAR-1999; 99US-0123957P;  
PR 17-AUG-1999; 99US-0146722P;  
PR 01-DEC-1999; 99US-014939P;  
PR 01-DEC-1999; 99WO-US028301;  
PR 16-DEC-1999; 99WO-US028634;  
PR 20-DEC-1999; 99WO-US030955;  
PR 05-JAN-2000; 2000WO-US00219;  
PR 06-JAN-2000; 2000WO-US00376;  
PR 11-FEB-2000; 2000WO-US03165;  
PR 18-FEB-2000; 2000WO-US004341;  
PR 22-FEB-2000; 2000WO-US004414;  
PR 24-FEB-2000; 2000WO-US004914;  
PR 24-FEB-2000; 2000WO-US005004.

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OM Protein - Protein search, using SW model

Run on: December 21, 2005, 13:26:47 ; Search time 38 Seconds  
(without alignments)

296.246 Million cell updates/sec

Title: US-10-659-782B-32

Perfect score: 620

Sequence: 1 MPSPGTVCSSLILGMWLDL.....PPSSRRRSRSHQPSCSPEL 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

#### Listing First 45 summaries

Database : PIR 80.0:  
 1: Pir1.\*  
 2: Pir2.\*  
 3: Pir3.\*  
 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	198		31.9	117	1 A59316	ghrelin precursor
2	158		25.5	117	1 A59316	ghrelin precursor
3	78		12.6	136	2 AG0449	regulator of nucle
4	73.0		11.9	2018	2 T34274	hypothetical prote
5	73		11.8	573	2 JC4335	anti-mullerian hor
6	73		11.8	725	1 B64211	virulence associat
7	72.5		11.7	555	2 HB3043	hypothetical prote
8	72		11.6	666	2 T2943	hypothetical prote
9	71.5		11.5	764	2 T48882	thyrotropin recept
10	70.5		11.4	309	2 S77905	lyase - Pseudomona
11	70.5		11.4	383	2 A66084	interleukin-1beta
12	69		11.1	302	2 H36792	unknown protein F1
13	69		11.1	1487	2 S62048	hypothetical membrane
14	68		11.0	796	2 T2425	retrotransposon li
15	68		11.0	1474	2 B85188	hypothetical prote
16	68		11.0	2088	2 E71436	thyrotropin recept
17	67.5		10.9	764	2 A31956	hypothetical prote
18	67		10.8	187	2 T51876	sensor protein Bas
19	67		10.8	363	2 F94265	sensor protein for
20	67		10.8	363	2 C86106	sensor protein bas
21	67		10.8	363	2 JX0285	hypothetical 51.8K
22	67		10.8	449	2 C39926	probable MYB famil
23	67		10.8	519	2 GB4707	interleukin-1beta
24	66.5		10.7	263	2 C56084	conserved hypothet
25	66.5		10.7	311	2 B56084	site-specific DNA
26	66.5		10.7	749	2 A75560	hypothetical prote
27	66		10.6	428	2 JH0634	bifunctional cycla
28	66		10.6	1001	2 T28897	
29	65.5		10.6	304	2 S25080	

#### ALIGNMENTS

#### RESULT 1

A59316

Ghrelin precursor - human

N;Alternate names: Preproghrelin

C;Species: Homo sapiens (man)

C;Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 09-Jul-2004

C;Accession: A59316

R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A;Reference number: A59316; PMID:20067939; PMID:10604470

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-117 <KOJ>

A;Cross-references: UNIPROT:Q9UBU3; UNIPARC:UPI0000362D3; GB:AB029434; NID:g6691571; PII

A;Experimental source: tissue stomach endocrine cells

A;Note: submitted to GenBank, June 1999

C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth

C;Superfamily: motilin

C;Keywords: hormone, lipoprotein, stomach

F;1-117 <KOJ> Product: Ghrelin #status Predicted <MAT>

F;52-117</domain: carboxyl-terminal propeptide #status Predicted <CTP>

F;26/Binding site: octanoate (Ser) (covalent) #status experimental

F;1-117 <KOJ> Product: Ghrelin #status Predicted <MAT>

F;52-117</domain: carboxyl-terminal propeptide #status Predicted <CTP>

Query Match Score 198; DB 113; Length 117;

Best Local Similarity 88.6%; Pred. No. 1.7e-13;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLGMLWLAMGSSFLSPLPHQVRVPRPKAP 44

Ds 1 MPSPGTVCSLLLGMLWLAMGSSFLSPLPHQVRVQRKESKCP 44

#### RESULT 2

B59316

Ghrelin precursor - rat

N;Alternate names: Preproghrelin

C;Species: Rattus norvegicus (Norway rat)

C;Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 09-Jul-2004

C;Accession: B59316

R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A;Reference number: A59316; PMID:20067939; PMID:10604470

A;Accession: B59316

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-117 <KOJ>

A;Cross-references: UNIPROT:Q9YH7; UNIPARC:UPI000012B411; GB:AB029431; NID:g6691569; PII

A;Experimental source: strain SD; tissue stomach endocrine cells

A;Note: submitted to GenBank, June 1999  
 C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone); lipoprotein; stomach  
 C;Keywords: hormone; lipoprotein; stomach  
 F;24-51/Domain: signal sequence #status predicted <SIG>  
 F;5-117/Domain: ghrelin #status predicted <MAT>  
 F;2/Binding site: octanoate (Ser) (covalent) #status experimental

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 Best Local Similarity 40.0%; Pred. No. 2.5e-09;  
 Matches 42; Conservative 7; Mismatches 34; Indels 22; Gaps 2;

Qy 1 MPSPERVCSULLGMWLDAMAGSSFLSDEHQLMASVPHKASHVPAAPLSNQLCDLE 60  
 Db 1 MVSATTCALLLSSLLSNWDDAMAGSSFLSDEHQLMASVPHKASHVPAAPLSNQLCDLE 60

Qy 61 QQRH-----LWASYSFSQTKDGSGLDTVSGRTWG 89  
 Db 55 GWLHPEDRGQAAEAEELERNAFEDVGTKLSQLGQYQGRALG 99

RESULT 5  
 JC4335  
 anti-mullerian hormone type II receptor precursor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 06-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 05-Oct-2004  
 C;Accession: JC4335  
 R;Visser, J.A.; McIuskey, A.; van Beers, T.; Wehuis, D.O.; van Kessel, A.G.; Grootegoed, Biochem. Biophys. Res. Commun. 215, 1029-1036, 1995  
 A;Title: Structure and chromosomal localization of the human anti-mullerian hormone type A;Reference number: JC4335; MUID:96028015; PMID:7488027

A;Accession: JC4335  
 A;Molecule type: mRNA  
 A;Residues: 1-573 <VIS>  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; White, A.; Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: HG0449  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-136 <KUR>  
 A;Cross-references: UNIPROT:Q8ZAU1; UNIPARC:UPI000000CABC; GB:AL590842; PIDN: CAC93163.1;  
 C;Genetics:  
 A;Gene: rnk

Query Match 12.6%; Score 78; DB 2; Length 136;  
 Best Local Similarity 26.2%; Pred. No. 0.64; Mismatches 39; Indels 26; Gaps 3;

Qy 21 AMAGS---SPSPEHQVRPHKASHVPAAPLSNQLCDLE-QQRLMASVPSQSTKD 76  
 Db 24 AFAGSYVATLINEELDRAELPPNEIPADVYTMNSRFLDNSEHIRTLYVPPSLKD 83

Qy 77 SGSDLTV-----SGRTWGLRVLNRLFPSS 101  
 Db 84 SNEQLSVMAPIGAALLGLHYNDEISWKLPQGDETRIVLLELYQPE 130

RESULT 4  
 T34274 hypothetical protein F46H5.4 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T34274  
 R;Nhan, M.  
 Submitted to the EMBL Data Library, November 1995  
 A;Description: The sequence of C. elegans cosmid F46H5.  
 A;Reference number: 22198  
 A;Accession: T34274  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Cross-references: UNIPROT:Q20487; UNIPARC:UPI0000081BE1; EMBL:U41543; PIDN:AAB37023.1;  
 A;Experimental source: strain Bristol N2; clone F46H5  
 C;Genetics:  
 A;Gene: CESP; F46H5.4

Qy 38 RPPHKAPHVVPALPLSNQLCDLEQQRHLMASVPSQSTKDGSQSDTIVS-GRTWGLRVLNR 95  
 Db 652 RTPHEFTDEIKLSP----CDLNDGHILLFTVHISCKEGDSSSTESPIGYTW----- 699

Qy 96 LFP--PSSRERSRSRSHQPS 113  
 Db 700 -LPLYRNGKLRSQGNFLPVC 718

RESULT 5  
 JC4335  
 anti-mullerian hormone type II receptor precursor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 06-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 05-Oct-2004  
 C;Accession: JC4335  
 R;Visser, J.A.; McIuskey, A.; van Beers, T.; Wehuis, D.O.; van Kessel, A.G.; Grootegoed, Biochem. Biophys. Res. Commun. 215, 1029-1036, 1995  
 A;Title: Structure and chromosomal localization of the human anti-mullerian hormone type A;Reference number: JC4335; MUID:96028015; PMID:7488027

A;Accession: JC4335  
 A;Molecule type: mRNA  
 A;Residues: 1-573 <VIS>  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; White, A.; Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: HG0449  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-136 <KUR>  
 A;Cross-references: UNIPROT:Q8ZAU1; UNIPARC:UPI000000CABC; GB:AL590842; PIDN: CAC93163.1;  
 C;Genetics:  
 A;Gene: rnk

Query Match 11.8%; Score 73; DB 2; Length 573;  
 Best Local Similarity 27.4%; Pred. No. 10; Mismatches 35; Indels 40; Gaps 6;

Qy 3 SPGTVCS-----LULGMLWLDLAMAGS---SFLSPHQVRVQVRP-PHKAP 44  
 Db 128 SPGPGSQGPQAANGESTINAVLGLFLULLVGSITALLQRKNYVRGEPPVPEPRP 187

Qy 45 H-----VVPALPLSNQLCDLEQQRHLMASVPSQSTKDGSQSDTIVS-GRTWGLRVLNR 97  
 Db 188 DSGRDWWSVBLQELP----ELC-----FSQVIREGGHAVWWAGOLQGKLVAIKAF 232

Qy 98 PPSS 101  
 Db 233 PPBS 236

RESULT 6  
 E64211 virulence-associated protein vacB homolog - Mycoplasma genitalium  
 C;Species: Mycoplasma genitalium  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: E64211  
 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.J.; Nguyen, D.; Utterback, T.R.; Sauder, D.M.; Phillips, C.A.; Merrick, J.C.; Venter, J.C.  
 A;Title: The minimal gene complement of Mycoplasma genitalium.  
 A;Reference number: A64200; MUID:96026346; PMID:7569993



C;Genetics:  
A;Gene: g1pB  
C;Superfamily: Pseudomonas pseudomallei lyase

Query Match 11.4%; Score 70.5; DB 2; Length 309;  
Best Local Similarity 22.0%; Pred. No. 9.6;  
Matches 29; Conservative 16; Mismatches 36; Indels 51; Gaps 5;

Qy 2 PSPGTYCSLJLGMLWDLAMAGSSFLSPEHORVQRPPKAPH-----VVPALEPLS 53  
Db 14 PEPGTIV-----LSGVTKRSRGRPPKAAYLARWKYSPITAAADPRA 53

Qy 54 NQLCDLQEQRHLWASYFSQSTKDSQSDLT-----VSGRTIWGL---RVLNRLFP 98  
Db 54 PQ-----HSWGNSRVDAADRERSTSKTRPNNSREEVVICMSFSSWNVNHEPRILNSQFA 105

Qy 99 PSSRERSRRSHQ 110  
Db 106 RKSLSNAAKPSHR 117

RESULT 11

A56084 interleukin-1beta converting enzyme beta isozyme - human  
C;Species: Homo sapiens (man)  
C;Accession: A56084  
R;Anemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.  
J. Biol. Chem. 270, 4312-4317, 1995  
A;Title: Cloning and expression of four novel isoforms of human interleukin-1beta converting enzyme: A56084; PMID:95181414; PMID:7876192  
A;Reference number: A56084  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-383 <ALN>  
A;Cross-references: UNIPROT:P29466;  
C;Genetics:  
A;Gene: IL1BCE  
C;Keywords: alternative splicing

Query Match 11.4%; Score 70.5; DB 2; Length 383;  
Best Local Similarity 22.0%; Pred. No. 12;  
Matches 27; Conservative 20; Mismatches 37; Indels 39; Gaps 4;

Qy 1 MPSPGTYCSLJLGMLWDLAMAGSSFLSPEHORVQRPPKAPHVVPALPLSN-----54  
Db 62 IPKGAGACQCITYCIBEDSYLAGTIGLSHAPQAQVDN-----PANTTSS-SSEBNV 112

Qy 55 QLCDLQEQRHLW---ASVFSQSTKDS-----GSPLTVSGRTWGL 90  
Db 113 KLCISLSEAQRWKQSAETIPIMDGSRSRTRLAIICTNEEFDSPRTGAVIDTGTMIL 172

Qy 91 RVL 93  
Db 173 QNL 175

RESULT 12

H96792 unknown protein F14G6.10 [Imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Accession: H96792  
R;Theologis, A.; Becker, J.R.; Palm, C.J.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anson, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Mazza, M.; Rooney, T.; Rowley, D.; Sakano, H.; Rizzo, M.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

T32425 hypothetical protein C10E2.3 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T32425  
 R:Wohldmann, P.; Sansone, J.  
 Submitted to the EMBL Data Library, September 1997  
 A;Description: The sequence of C. elegans cosmid C10E2.  
 A;Reference number: 221165  
 A;Accession: T32425  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-736 <W01>  
 A;Cross-references: UNIPARC:UPI000075F65; EMBL:AF026202; PIDN:AAB71243.  
 A;Experimental source: strain Bristol N2; clone C10E2  
 C;Genetics:  
 A;Gene: CESP::C10E2.3  
 A;Map Position: X  
 A;Introns: 85/2; 220/2; 269/1; 305/1; 519/3; 576/3; 724/3; 755/3  
 Query Match 11.0%; Score 68; DB 2; Length 796;  
 Best Local Similarity 28.6%; Pred. No. 50;  
 Matches 28; Conservative 15; Mismatches 35; Indels 20; Gaps 4;  
 Qy 18 LDLMAGGSFLSPSPHQRVQV-RPPHKAPHVVPALPLSNQLCDLEQQRHILMASVPSQSTD 76  
 Db 47 LSLANLTNLSSSGNLNSVQPQTKEH-PTAPTSNRKCDLPRSN--SNTTSQLTKD 101  
 Qy 77 SGSDLTVSGRTWGLRVLNRLFPSSRRSRSSHOPSCS 114  
 Db 102 -----RLKNNIANRSKGESNSQSNLMSNS 125

RESULT 15  
 B85188 retrotransposon like protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C;Accession: B85188  
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999  
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A;Reference number: A85001; MUID:20083488; PMID:10617198  
 A;Accession: B85188  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1474  
 A;Cross-references: UNIPROT:O232529; UNIPARC:UPI0000A464B; GB:NC\_001268; NID:95302802; E  
 C;Genetics:  
 A;Gene: d1465C  
 A;Map Position: 4  
 C;Superfamily: retrovirus-related polyprotein

Query Match 11.0%; Score 68; DB 2; Length 1474;  
 Best Local Similarity 27.0%; Pred. No. 99;  
 Matches 30; Conservative 19; Mismatches 42; Indels 20; Gaps 5;  
 Qy 71 SQSTKD-----SGSDLTIVSGRTWGLRVLNRLFPSSRRSRSSHOPSCSP 115  
 Db 767 EQSSPLVTPLSSSVLSCLSSCTVLUQQQPPTTPNPSHSQPTTSP 817  
 Qy 716 VFLCQSLQTAYLDPDVKRKL-----YNSRHVYFDEASPFNSN--LTSQNQSPVTFP 766

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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- [1] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), AND ACYLATION OF SER-26.  
RC TISSUE=Stomach;  
RX MEDLINE=20067939; PubMed=10604470; DOI=10.1038/45230;  
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;  
RT "Ghrelin is a growth-hormone-releasing acylated peptide from  
RT stomach.";  
RL Nature 402:656-660 (1999).  
RN [2]
- RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33.  
RT TISSUE=stomach;  
RX MEDLINE=20389976; PubMed=10930375;  
RA Tomasetto C., Karan S.M., Ribieras S., Masson R., Lefebvre O.,  
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;  
RT "Identification and characterization of a novel gastric peptide  
RT hormone: the motilin-related peptide.";  
RL Gastroenterology 119:1395-405 (2000).  
RN [3]
- RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RA Wajnrajch M.P., Ten I.S., Gerritt J.M., Leibl R.L.;  
RT "Genomic organization of the human Ghrelin gene.";  
RL J. Endocr. Genet. 1:231-233 (2000).  
RN [4]
- RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2), TISSUE SPECIFICITY, ACYLATION  
OF SER-26, AND MASS SPECTROMETRY.  
RX Pubmed=1214809; DOI=10.1074/1bc.M205366200;  
RA Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;  
RT "Structural diversity of human Ghrelin. Identification of multiple  
RT Ghrelin-derived molecules produced by post-translational processing.";  
RL Biol. Chem. 278:64-70 (2003).  
RN [5]
- RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RX MEDLINE=22887296; PubMed=12973309; DOI=10.1101/gr.1291003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deusei B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimek L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R.L., Watanabe C., Wiesand D., Woods K., Xie M.H.,  
RA Yansura D.G., Yi S., Yu G., Zhang J., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270 (2003).  
RN [6]
- RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RT TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=124797932; DOI=10.1073/pnas.242603899;
- RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausmeier R.D., Collins F.S., Wagner L., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J.,  
RA Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakely R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
RA Scherich A., Schein J.E., Jones S.J.M., Mirza M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [7]
- RP PROTEIN SEQUENCE OF 24-38.

- RX PubMed=15340161; DOI=10.1110/pb.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites";  
RA Protein Sci. 13:2819-2824 (2004).  
RN [8]
- RP REVIEW.  
RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;  
RA Kojima M., Hoorda H., Matsuo H., Kangawa K.;  
RT "Ghrelin: discovery of the natural endogenous ligand for the growth  
hormone secretagogue receptor.";  
Trends Endocrinol. Metab. 12:118-122 (2001).  
CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue  
receptor type 1 (GHSR) inducing the release of growth hormone from  
the pituitary. Has an appetite-stimulating effect, induces  
adiposity and stimulates gastric acid secretion. Involved in  
growth regulation.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=;; Synonyms=Ghrelin;  
CC Isobid=QUBU3-1; Sequence=Displayed;  
CC Name=2;; Synonyms=dai-Gln14-ghrelin;  
CC Isobid=QUBU3-2; Sequence=VS\_P\_003245;  
CC -|- TISSUE SPECIFICITY: Highest level in stomach. All forms are found  
in serum as well. Other tissues compensate for the loss of ghrelin  
synthesis in the stomach following gastrectomy.  
CC -|- PTM: O-n-octanoylation is essential for activity. The O-n-  
deacylated forms Ghrelin-27-C10 and Ghrelin-28-C10 differ in the  
length of the carbon backbone of the carboxylic acid bound to Ser-  
26. A small fraction of Ghrelin, Ghrelin-28-C10, may be modified  
with an unsaturated carboxylic acid.  
CC -|- MASS SPECTROMETRY: MW=3398.9; MW\_BER=0.3; METHOD=Electrospray;  
CC Range=24-51 (Ghrelin-28-C10); NOTE=O-deacylated form (Ref 4).  
CC -|- MASS SPECTROMETRY: MW=3397.2; MW\_BER=0.5; METHOD=Electrospray;  
CC Range=24-51 (Ghrelin-28-C10); NOTE=O-deacylated form (Ref. 4).  
CC -|- MASS SPECTROMETRY: MW=3371.3; MW\_BER=0.1; METHOD=Electrospray;  
CC Range=24-51 (Ghrelin-28-C10); NOTE=O-octanoylated form (Ref. 4).  
CC -|- MASS SPECTROMETRY: MW=3243.6; MW\_BER=0.1; METHOD=Electrospray;  
CC Range=24-50 (Ghrelin-28-C10); NOTE=O-deacylated form (Ref 4).  
CC -|- MASS SPECTROMETRY: MW=3214.6; MW\_BER=0.6; METHOD=Electrospray;  
CC Range=24-50 (Ghrelin-27); NOTE=O-octanoylated form (Ref. 4).  
CC -|- SIMILARITY: Belongs to the motilin family.  
CC -|- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
WWW=<http://www.intcibio.fr/services/chromcancer/Genes/GhrelinID327.html>.  
CC ---  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC use as long as its content is in no way modified and this statement is not  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC ---  
DR AB029434; BA89371.1; -; mRNA.  
DR AJ252278; CAB673.1; -; mRNA.  
DR AF296558; AAC10301.1; -; Genomic\_DNA.  
DR AB035700; BAB19045.1; -; mRNA.  
DR EMBL; AY359052; AA089412.1; -; mRNA.  
DR PIR; A59316; A59316.  
DR PDB; 1PTX; Model; A=1-117.  
DR EnSG0000157017; Homo sapiens.  
DR H-InvDB; HIX0003050; -.  
DR MIM; 60553; -.  
DR GO; GO:0005615; C:extracellular space; ISS.  
DR GO; GO:001664; F:G-protein-coupled receptor binding; ISS.  
DR GO; GO:001668; F:growth hormone-releasing hormone activity; ISS.  
DR GO; GO:0007185; P:G-protein coupled receptor protein signalin. . . ; ISS.  
DR InterPro; IPR006737; motilin\_assoc.  
DR InterPro; IPR006738; motilin\_Ghrelin.  
DR InterPro; IPR05441; ProgGhrelin.  
DR PANTHER; PTMR4122; ProgGhrelin\_1.  
DR Pfam; PF04643; Motilin\_assoc; 1.

DR	Pfam; PF04644; Motilin ghrelin; 1.							
PRINTS	PR01624; GRELIN							
ProDom	PD332162; Preproghrelin; 1.							
KW	3D-structure; Alternative splicing; Direct protein sequencing;							
Hormone; Lipoprotein; Signal;								
SIGNAL	1 23							
FT	Ghrelin-28.							
PEPTIDE	24 51							
FT	Ghrelin-27.							
PROPEP	24 50							
FT	Removed in mature form.							
LIPID	26 26	O-decanoyl serine (in form ghrelin-27-C10 and form ghrelin-28-C10).						
LIPID	26 26	O-octanoyl serine (in form ghrelin-27 and form ghrelin-28).						
FT	Missing (in isoform 2).							
FT	/FTid=VSP_003245.							
CONFLICT	72 72 L -> M (in Ref. 6).							
SQ	SEQUENCE 117 AA; 12911 MW; 390C0572BEECA2755 CRC64;							
Query Match	31.9%; Score 198; DB 1; Length 117;							
Best Local Similarity	88.6%; Pred. No. 1. 4e-12;							
Matches	39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;							
AC	Q6UDF7_MACMU PRELIMINARY;	PRT; 117 AA.						
Q6UDF7	Q6UDF7_MACMU PRELIMINARY;	PRT; 117 AA.						
AC	Q6UDF7; 05-JUL-2004 (TREMBrel. 27, Created)							
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)							
DT	01-PB-2005 (TREMBrel. 29, Last annotation update)							
DB	Ghrelin; Name=GHLR;							
OS	Macaca mulatta (Rhesus macaque).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.							
NCBI_TaxID	9544; [1]							
RN								
RP	NUCLEOTIDE SEQUENCE.							
RR	PubMed-14736731; DOI=10.1210/en.2003-1103; Angelioni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J., Suomi S., Hansen B.C.; "Characterization of the rhesus monkey ghrelin gene and factors influencing ghrelin gene expression and fasting plasma levels.";							
RA	Endocrinology 145:2197-2205 (2004).							
RL	EMBL; AY37274; AAQ74837.1; -; Genomic_DNA.							
DR	EMBL; AY37274; AAQ74837.1; -; mRNA.							
DR	GO: GO:0005576; C:extracellular region; IEA.							
DR	GO: GO:0016608; F: growth hormone-releasing hormone process; IEA.							
DR	GO: GO:0050791; P: regulation of physiological process; IEA.							
DR	InterPro; IPR006737; motilin_assoc.							
DR	InterPro; IPR006738; preproghrelin.							
DR	PANTHER; PTHR14122; Preproghrelin; 1.							
PFam	PF0643; Motilin_assoc; 1.							
DR	PF04644; Motilin_ghrelin; 1.							
PRINTS	PR01624; GRELIN.							
ProDom	PD332162; Preproghrelin; 1.							
SQ	SEQUENCE 117 AA; 12913 MW; 1B64ACB1E1F19FF CRC64;							
Query Match	31.3%; Score 194; DB 2; Length 117;							
Best Local Similarity	86.4%; Pred. No. 3.5e-12;							
Matches	38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;							
CC	Event-Alternative Splicing; Named isoform=2;							
CC	Name=; Synonyms=Ghrelin;							
CC	Isoid=QBEBG6-1; Sequence=Displayed;							
CC	Name=2; Synonyms=de1_Gln14-Ghrelin;							
CC	Isoid=Q66B6-2; Sequence=VSP_011616;							
CC	- PTM: O-n-octanoylation is essential for activity (By similarity).							
CC	- SIMILARITY: Belongs to the motilin family.							

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**InterPro:** IPR005441; **Preproghrelin**.  
**PANTHER:** PTHR14\_122; **Preproghrelin**; 1.  
**Pfam:** PF004643; Motilin assoc.; 1.  
**Pfam:** PF004644; Motilin ghrelin; 1.  
**PRINTS:** PRO1644; **GRELIN**.

DR	InterPro; IPR005441; Proprghrelin.
DR	PANTHER; PTHR4122; Preproghrelin; 1.
DR	Pfam; PF04643; Motilin_assoc; 1.
DR	Pfam; PF04644; Motilin_ghrelin; 1.
PRINTS	PRO1644; GHRELIN.
DR	ProDom; PD332162; Preprghrelin; 1.
KW	Hormone; Lipoprotein; Signal.
FT	SIGNAL 23 By similarity.
FT	PEPTIDE 1 Ghrain (By similarity).
FT	PROTEIN 24 50 Removed in mature form (By similarity).
FT	PROPP 51 116 O-octanoyl serine (By similarity).
FT	LIPID 26 26
SQ	SEQUENCE 116 AA; 12935 MW; CDA6797/D72E303 CRC64;
Query Match	27 7% ; Score 171.5; DB 1; Length 116;
Best Local Similarity	42.9% ; Pred. No. 7.6e-10;
Matches	42; Conservative 13; Mismatches 34; Indels 9; Gaps 2
Qy	1 MPSPGTVCSULLGMLWDLAMAGSSFLSPEHQYVQRPHKAPHVVPALPLSNQL CDL 59
Db	1 MPAPRTICSULLSLWMDLAMAGSSFLSPEHQYVQRPHKAPHVVPALPLSNQL CDL 60
Qy	60 EQQRH-----LWASVFSQSTKDGSQDSLTVSGTWG 89
Db	61 GSQEFGADELEIRNAPFNIGKISGAQLQHGGTQLG 98
RESULT 7	
Q8CH53_MERUN_ID	Q8CH53_MERUN PRELIMINARY; PRT; 117 AA.
AC	Q8CH53;
DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Ghrelin prepropeptatin.
OS	Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Gerbillinae; Gerbillines.
OX	NCBItaxID=10047;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	EMBL: AF442491; AA006965.1; -; mRA.
RA	Suzuki H., Maeda T., Hosoda H., Ota T., Minegishi Y., Nomura S., Kanbara K., Ishii H.;
RA	"Helicobacter pylori infection modifies gastric and plasma ghrelin dynamics in Mongolian gerbils.";
RT	Gut 53:187-194 (2004).
RL	InterPro; IPR006737; motilin_assoc.
DR	InterPro; IPR005441; Preproghrelin.
DR	PANTHER; PTHR4122; Preproghrelin; 1.
DR	Pfam; PF04643; Motilin_assoc; 1.
DR	Pfam; PF04644; Motilin_ghrelin; 1.
PRINTS	PRO1644; GHRELIN.
DR	ProDom; PD332162; Preprghrelin; 1.
SQ	SEQUENCE 117 AA; 13035 MW; 275568/FC023A74 CRC64;
Query Match	26.6% ; Score 165; DB 2; Length 117;
Best Local Similarity	41.0% ; Pred. No. 3.7e-09;
Matches	43; Conservative 8; Mismatches 32; Indels 22; Gaps 2
Qy	1 MPSPTVCSULLGMLWDLAMAGSSFLSPEHQYVQRPHKAPHVVPALPLSNQLCDL 60
Db	1 MMSSTTCSULLGLWDLAMAGSSFLSPEHQYVQRPHKAPHVVPALPLSNQLCDL 64

EMBL: AB009200; BAD34669.1; -; mRNA.  
InterPro: IPR006737; motilin\_assoc.  
InterPro: IPR006738; motilin\_gbrel.

61 QQRH-----LWASVFSQSTKIDSLTVSGRIVW 89  
 55 GWLHPDGRQAGAEDELFIRFNAPPDVGILKLSSGAQYODHRGALG 99

**RESULT 8**

**GHRL MOUSE STANDARD:** PRT; 117 AA.

AC Q9EQX0; Q9WZU1; (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DB Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).

GN Name=Chr1; Synonyms=Mt1rP;

OS Mus musculus (Mouse).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinidae; Murinidae.

OX NCBI\_TaxID=10050;

RN [1] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF TISSUE=Stomach; RC: Sequence=Displayed;

RX MEDLINE=203899/6; PubMed=10930375;

RA Staub A., Karim S.M., Ribieras S., Masson R., Lefebvre O., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; RLT Gastroenterology 119:395-405(2000).

[2] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1). RA Kojima M.; "Mouse mRNA for preproghrelin."; RLT Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

[3] NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM 1). RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakashima K.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE MENA] (ISOFORM 1). RC STRAIN=C57BL/6J; TISSUE=Stomach; MEDLINE=23354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bonci H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H., Tomaru Y., Yagi K., Tomaru Y., Hasegawa Y., Nagami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matauda H., Batalov S., Beigel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dragani T.A., Fletcher C.F., Forrest J., Gough J., Godzik A., Gough J., Jackson I.J., Jarvis E.D., Gaasterland T., Garibaldi M., Gissi C., Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Magioli D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okada T., Pavani W.J., Peretz G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.D., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultan R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wu J., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hiroseane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573 (2002).

[5] DB DEVELOPMENTAL STAGE, AND ACYLATION OF SPB-26. RX PubMed=157446259; DOI=10.1210/en.2004-0645;

RA Nishi Y., Hiejima H., Mifune H., Sato T., Kangawa K., Kojima M.; RT "Developmental changes in the pattern of ghrelin's acyl modification

and the levels of acyl-modified ghrelin in murine stomach.";

[6]

RT REVIEW; PMID=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;

RX Kojima M., Hosoda H., Matsuo H., Kangawa K.; "Ghrelin: discovery of the natural endogenous ligand for the growth hormone secretagogue receptor.";

RT Trends Endocrinol. Metab. 12:118-122 (2001).

DB -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=Ghrelin; IboID=Q9QQX0-1; Sequence=del.Gln14-Ghrelin;

CC Name=2; Synonyms=del.Gln14-Ghrelin; IboID=Q9BXO-2; Sequence=VSP\_003246;

CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract with higher levels in the stomach, medium levels in the duodenum, jejunum, ileum and colon. Low expression in the testis and brain.

CC Not detected in the salivary gland, pancreas, liver and lung.

CC -!- DEVELOPMENTAL STAGE: Levels of n-octanoylated and n-decanoylated ghrelin drop by one third and 3-fold, respectively, between postnatal weeks 3 and 4 due to change of diet during weaning.

CC -!- PTM: O-n-octanoylation is essential for activity (By similarity). The O-n-decanoylated form ghrelin-COO differs in the length of the carbon backbone of the carboxylic acid bound to Ser-26.

CC -!- SIMILARITY: Belongs to the motilin family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC DR EMBL: AB015701; BAB19046\_1; -; mRNA.

CC DR EMBL: AB08658; BAB2957\_1; -; Genomic\_DNA.

CC DR EMBL: AK008860; BAB25934\_1; -; mRNA.

CC DR Ensembl: BNSMDSG000064177; Mus musculus.

CC DR MGI: MGI\_1930008; Ghrl.

CC DR GO: GO\_0005737; C:cytoplasm; IDA.

CC DR GO: GO\_0005615; C:extracellular space; TAS.

CC DR InterPro: IPR006737; motilin\_assoc.

CC DR InterPro: IPR006738; motilin\_Ghrelin.

CC DR InterPro: IPR005441; Preproghrelin.

CC DR PANTHER: PTHR4122; Preproghrelin.

CC DR Pfam: PF00643; Motilin\_assoc; 1.

CC DR Pfam: PF04644; Motilin\_ghrelin; 1.

CC DR PRINTS: PR01624; GHRELIN.

CC DR ProdDom: PD332162; Preproghrelin; 1.

CC KW Alternative splicing; Direct protein sequencing; Hormone; Lipoprotein; Signal.

CC FT SIGNAL 1 23

CC FT PEPTIDE 24 51

CC FT PROTEIN 52 117

CC FT LIPID 26 26

CC FT VARSPLIC 37 37

CC SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;

Query Match 26.3%; Score 163; DB 1; Length 117;

Best Local Similarity 41.0%; Pred No. 5.9e-09;

Matches 43; Conservative 7; Mismatches 33; Indels 22; Gaps 2;

Qy 1 MPSPGTVCSLILGMLWLAMAGSSFLSPHEQRYVQVRPHKAPVVPALPLSNOLCDE 60  
Db 1 MLLSGTICSLLSMWMAMAGSSFLSPHQKAQQRKESKKP-----PAKLOPRALE 54

Qy 61 QQRH-----LWASVFSQSTKDSGLTIVSGRTWG 89  
Db 5 GWLHPEDRGQAETEEBELEIRFNAPPDVGIXLGSQYQHQGRALG 99

RESULT 9  
Q81174\_MOUSE PRELIMINARY; PRT; 86 AA.  
ID Q81174\_MOUSE PRELIMINARY;  
AC DT 01-JUN-2003 (T-REMBLrel. 24, Created)  
DT 01-JUN-2003 (T-REMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (T-REMBLrel. 26, Last annotation update)  
DE Exon 4-deleted preproghrelin variant.  
GN Name=Chrl;  
OS Mus musculus (Mouse);  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muriniae; Mus.  
NCBI\_TaxID=10030;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sus98;  
RX PubMed=15471962; DOI=10.1210/en.2003-1446;  
RA Jeffrey P.L., Duncan R.P., Yeh A.H., Jaskolski R.A., Hammond D.S.,  
RA Herrington A.C., Chopin L.K.,  
RT "Expression of the ghrelin axis in the mouse: exon 4-deleted mouse  
proghrelin variant encodes a novel C terminal peptide.",  
RL Endocrinology 146:412-440(2005).  
DR EMBL; AY17930; AA027350.1; -; mRNA.  
DR Ensembl; ENSMUSG00000064177; Mus musculus.  
DR MGI; MGI:1930008; Ghrl.  
DR GO:005727; :cytoplasm; IDA.  
DR GO:0005615; C:extracellular space; TAS.  
DR GO:0005179; F:hormone activity; TAS.  
DR InterPro; IPR06738; motilin.  
DR InterPro; IPR00544; Preproghrelin.  
DR PANTHER; PTHR14122; Preproghrelin; 1.  
DR Pfam; PF0644; Motilin\_assoc; 1.  
DR PRODOM; PD332262; Preproghrelin; 1.  
DR PRIONER; PTHR14122; Preproghrelin; 1.  
DR SIGNAL; PRO1624; GHRELIN.  
SQ PEPRINTS; B913858874770512 CRC64;  
SEQUENCE 86 AA; 9758 MW;

Query Match 26.1%; Score 162; DB 2; Length 86;  
Best Local Similarity 70.5%; Pred. No. 5.2e-09;  
Matches 31; Conservative 4; Mismatches 9; Indels 0; Gaps 0; Gaps 0;

Qy 1 MPSPGTVCSLILGMLWLAMAGSSFLSPHEQRYVQVRPHKAP 44  
Db 1 MLLSGTICSLLSMWMAMAGSSFLSPHQKAQQRKESKKP 44

RESULT 10  
GHRL\_CANFA STANDARD; PRT; 117 AA.  
ID Q9BEP7; Q9BEP7;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone  
releasing peptide) (Motilin-related peptide).  
GN Name=GHRL; Synonyms=MTLRP;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora;  
OC Canis.  
NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (mRNA) (ISOFORMS 1 AND 2).  
RC TISSUE=Gastric fundus.

RA Tomassetto C., Wendling C., Rio M.-C., Poitras P.;  
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog  
funding.";  
RL Submitted (JAN 2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).  
RC TISSUE=Stomach;  
RC TISSUE="Dog, Kojima M., Hosoda H., Kajiya H., Matsuo H., Kangawa K.;"  
RA RT "Dog Ghrelin."  
RL Submitted (APR 2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: specific ligand for the growth hormone secretagogue  
CC receptor type 1 (GHSR) inducing the release of growth hormone from  
CC the pituitary. Has an appetite-stimulating effect, induces  
CC adiposity and stimulates gastric acid secretion. Involved in  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS: Secreted.  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=Ghrelin;  
CC Isoid=Q9BEP8-1; Sequence=Del\_Gln14=Ghrelin;  
CC Name=2; Synonyms=del\_Gln14=Ghrelin;  
CC Isoid=Q9BEP8-2; Sequence=VSP\_003344;  
CC -1- PTM: O-n-octanoyl group; Activity=VSP\_003344;  
CC -1- SIMILARITY: Belongs to the motilin family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC DR AJ298295; AAC29155.1; -; mRNA.  
DR EMBL; AJ298296; AAC29156.1; -; mRNA.  
DR AB060700; BAC75929.1; -; mRNA.  
DR Ensembl; ENSCARG000000000129; Canis familiaris.  
DR InterPro; IPR006737; motilin assoc.  
DR InterPro; IPR006738; motilin.  
DR InterPro; IPR005441; Preproghrelin.  
DR PANTHER; PTHR14122; Preproghrelin; 1.  
DR Pfam; PF04643; Motilin\_assoc; 1.  
DR Pfam; PF0644; Motilin; 1.  
DR PRINTS; PR01624; GHRELIN.  
DR PRODOM; PD332262; Preproghrelin; 1.  
DR PRIONER; PTHR14122; Preproghrelin; 1.  
DR SIGNAL; PRO1624; GHRELIN.  
KW Alternative splicing; Hormone; Lipoprotein; Signal.  
FT SIGNAL 1 23 BY similarity.  
FT GHREIN 1 51 BY similarity.  
FT Removed in mature form (By similarity).  
FT PROPEP 24 51 GHREIN (By similarity).  
FT LIPIP 52 117 Removed in mature form (By similarity).  
FT VARSPIC 26 26 O-acyanoyl serine (By similarity).  
FT FTID-VSP\_003344. 37 37 Missing (in isoform 2).  
FT SEQUENCE 117 AA; 13007 MW; 3E57FEDD184CF7 CRC64;  
FT SEQ 1 23 BY similarity.  
Query Match 26.1%; Score 162; DB 1; Length 117;  
Best Local Similarity 70.5%; Pred. No. 7.5e-09;  
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLILGMLWLAMAGSSFLSPHEQRYVQVRPHKAP 44  
Db 1 MPSLGTMCSLILFSVLWLAMAGSSFLSPHQKAQQRKESKKP 44

RESULT 11  
Q7TSD1\_MOUSE PRELIMINARY;  
ID Q7TSD1; AC Q7TSD1;  
DT 01-OCT-2003 (T-REMBLrel. 25, Created)  
DT 01-OCT-2003 (T-REMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (T-REMBLrel. 26, Last annotation update)  
DB Ghrelin delta2.  
GN Name=GHRL; Synonyms=Ghrelin;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora;  
OC Canis.  
NCBI\_TaxID=9615;



Best Local Similarity 40.0%; Pred. No. 2e-08; Matches 42; Conservative 7; Mismatches 34; Indels 22; Gaps 2;	OX RN NCBI_TaxID=9823;
AC RN NUCLEOTIDE SEQUENCE.	RP
RA Kim K.-S., Rothschild M.F.;	RT "Pig Ghrelin."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.	DR GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.	DR GO; GO:00050791; P:regulation of physiological process; IEA.
DR InterPro; IPR006738; motilin_grehelin.	DR InterPro; IPR005441; Progrehelin.
DR PANINTER; PTHR14122; Preproghrelin; 1.	DR PANINTER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04644; Motilin_grehelin; 1.	DR Prints; PRO1624; GHRELIN.
DR PT NON_TER 74 AA; 7980 MW; 875424C2D41FC166 CRC64;	DR PT NON_TER 74 AA; 7980 MW; 875424C2D41FC166 CRC64;
DT SQ	Query Match 24.3%; Score 150.5%; DB 2; Length 74;
DT DT Best Local Similarity 71.1%; Pred. No. 6.8e-08;	Matches 32; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
DT DR DE	Qy 1 MPSPGTVCSLLLGMLWL-DIAMASSSFLSPEHQYQVRPHKAP 44
OS OC 1 MPSTGTCISLLLSVLLMADLAMASSFLSPEHQYQVRKESKKP 45	Db 1 MPSTGTCISLLLSVLLMADLAMASSFLSPEHQYQVRKESKKP 45
RN [1]	
RP NUCLEOTIDE SEQUENCE.	RESULT 15
RC TISSUE-Stomach; RA GHRL_PIG STANDARD; PRT; 118 AA.	GHRL_PIG STANDARD; PRT; 118 AA.
RA Doi K., Kojima M., Hosoda H., Kawai H., Matsuo H., Kangawa K.;	AC Q9GKX5; Q9BDG8; Q9GKY4;
RT "sheep Ghrelin "	AC Q9GKX5; Q9BDG8; Q9GKY4;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR EMBL; AB06599; BAC05928.1; " mRNA.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR GO; GO:0005576; C:extracellular region; IEA.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR InterPro; IPR006737; motilin_assoc.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR IPR006738; motilin_grehelin.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR PANINTER; PTHR14122; Preproghrelin.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR Pfam; PF04643; Motilin_assoc; 1.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR Prints; PRO1624; GHRELIN.	AC Q9GKX5; Q9BDG8; Q9GKY4;
DR Prodrom; PD332162; Preproghrelin; 1.	AC Q9GKX5; Q9BDG8; Q9GKY4;
KW SIGNAL	CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
FT CHAIN 24 50 Potential.	CC -1- ALTERNATIVE PRODUCTS:
FT SQ SEQUENCE 116 AA; 12977 MW; B78EEA3DBF0E560E CRC64;	CC Name=-; Synonyms=Ghrelin;
Query Match 25.4%; Score 157.5%; DB 2; Length 116;	CC Isoid=Q9GKX5-1; Sequence=Displayed;
Best Local Similarity 40.8%; Pred. No. 2.2e-08; Matches 40; Conservative 14; Mismatches 35; Indels 9; Gaps 2;	CC Name=2; Synonyms=de-1-Gln14_grehelin;
Qy 1 MPSPGTVCSLLLGMLWL-DIAMASSSFLSPEHQYQVRPHKAP 59	CC Isoid=Q9GKX5-2; Sequence=VSP 003247;
Db 1 MPATPTTYSLLLSVLLMADLAMASSFLSPEHQYQVRKESKKP 60	CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
Qy 60 EQQRH-----Lwasyfsqstkdsgsdltysgrtwg 89	CC -1- SIMILARITY: Belongs to the motilin family.
Db 61 GSQEEGAEDELIRNAFPNIGIKLSSQSLQHGQTLG 98	CC -1- SIMILARITY: This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
RESULT 14	CC DR AB035703; BAB19048.1; mRNA.
ID Q77BBS_PIG PRELIMINARY; PRT; 74 AA.	CC
AC Q77BBS_PIG PRELIMINARY; PRT; 74 AA.	CC
DT 25-OCT-2004 (TrEMBLrel. 28, Created)	CC
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	CC
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	CC
DB Grehelin (Fragment).	CC
OS Sus scrofa (Pig).	CC
OC Mammalia; Chordata; Craniata; Vertebrata; Cetartiodactyla; Suiidae;	CC
OC Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suiidae;	CC
OC Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suiidae;	CC



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Qy 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRPHKAP 44  
 Db 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRKESKKP 44

RESULT 2  
 US-08-822-897C-2  
 ; Sequence 2, Application US/08822897C  
 ; Patent No. 6380138  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Deisher, Theresa A.  
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; STATE: Seattle  
 ; COUNTRY: WA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; APPLICATION NUMBER: US/08/822, 897C  
 ; FILING DATE:  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sawislak, Deborah A.  
 ; REGISTRATION NUMBER: 37,438  
 ; REFERENCE/DOCKET NUMBER: 91-04  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6672  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 117 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-822-897C-2

Query Match 31.9%; Score 198; DB 2; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 4e-17;  
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRPHKAP 44  
 Db 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRKESKKP 44

RESULT 3  
 US-09-608-810A-4  
 ; Sequence 4, Application US/0960810A  
 ; Patent No. 6420521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Jaspers, Stephen R.  
 ; APPLICANT: Bishoff, Paul D.  
 ; TITLE OF INVENTION: SGIP PEPTIDES  
 ; FILE REFERENCE: 99-51  
 ; CURRENT APPLICATION NUMBER: US/09/608, 810A  
 ; CURRENT FILING DATE: 2000-06-30

Query Match 31.9%; Score 198; DB 2; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 4e-17;  
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRPHKAP 44  
 Db 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRKESKKP 44

RESULT 4  
 US-09-404-417A-2  
 ; Sequence 2, Application US/09404417A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; PATENT NO. 6627729  
 ; APPLICANT: Deisher, Theresa A.  
 ; APPLICANT: Jaspers, Stephen R.  
 ; TITLE OF INVENTION: TML PEPTIDES  
 ; FILE REFERENCE: 97-04C1  
 ; CURRENT APPLICATION NUMBER: US/09/404, 417A  
 ; CURRENT FILING DATE: 1999-09-23  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 117  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-404-417A-2

Query Match 31.9%; Score 198; DB 2; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 4e-17;  
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRPHKAP 44  
 Db 1 MPSPGTVCSLLLGMLWLDAAGSSFLSPEHQRYVQRKESKKP 44

RESULT 5  
 US-09-794-987-2  
 ; Sequence 2, Application US/09794987  
 ; Patent No. 6838138  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS SEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/794,987  
 FILING DATE: 27-Feb-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sisilak, Deborah A.  
 REGISTRATION NUMBER: 37,438  
 REFERENCE/DOCKET NUMBER: 97-04  
 TELEPHONE: 206-442-6672  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-794-987-2

Query Match 31.9%; Score 198; DB 2; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 4e-17; 5; Indels 0; Gaps 0;

Qy	1	MPSPGTVCSLLLGMLWLDLAMAGSSPLSPBHQVRPQVRPHKAP 44
Db	1	MPSPGTVCSLLLGMLWLDLAMAGSSPLSPBHQVRPQVRKESKKP 44

RESULT 6

US-09-853-253-2

Sequence 2, Application US/09853253  
 Parent No. 6897286  
 GENERAL INFORMATION:  
 APPLICANT: JASPER, STEPHEN  
 APPLICANT: SHEPPARD, PAUL  
 APPLICANT: DEISHER, THERESA  
 APPLICANT: BISHOP, PAUL  
 TITLE OF INVENTION: Zs1933-like Peptides  
 FILE REFERENCE: 00-30  
 CURRENT APPLICATION NUMBER: US/09/853,253  
 CURRENT FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 60/203,300  
 PRIOR FILING DATE: 2000-05-11  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 117  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-853-253-2

Query Match 31.9%; Score 198; DB 2; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 4e-17; 5; Indels 0; Gaps 0;

Qy	1	MPSPGTVCSLLLGMLWLDLAMAGSSPLSPBHQVRPQVRPHKAP 44
Db	1	MPSPGTVCSLLLGMLWLDLAMAGSSPLSPBHQVRPQVRKESKKP 44

RESULT 7

US-09-991-181-268

Sequence 268, Application US/0991181  
 Patent No. 6933919  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.

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; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090435
;
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
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; PRIOR APPLICATION NUMBER: 60/090863
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;
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Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 8
US-09-990-444-268
; Sequence 268, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; Sequence 268, Application US/09990444
; Applicant: Ashkenazi, Avi J.
; Applicant: Baker, Kevin P.
; Applicant: Botstein, David
; Applicant: Destroyers, Luc
; Applicant: Eaton, Dan L.
; Applicant: Ferrara, Napoleone
; Applicant: Fong, Sherman
; Applicant: Gerber, Hanspeter
; Applicant: Gerritsen, Mary E.

```

APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Klijavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James B.  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic acids Encoding the Same  
 FILE REFERENCE: P2730P1C19

CURRENT APPLICATION NUMBER: US/09/990,444  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106

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 PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087609

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 PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088025

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 PRIOR APPLICATION NUMBER: 60/088029

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 PRIOR APPLICATION NUMBER: 60/088326

PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088167

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 PRIOR APPLICATION NUMBER: 60/090445

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 PRIOR FILING DATE: 1998-07-01  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/796,158  
 FILING DATE: 28-Feb-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION NUMBER: 09/046,479  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sawislak, Deborah A.  
 REGISTRATION NUMBER: 37,438  
 REFERENCE/DOCKET NUMBER: 97-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6672  
 TELEFAX: 206-442-6678  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-796-158-2

Query Match 31.9%; Score 198; DB 2; Length 117;  
 Best Local Similarity 88.6%; Pred. No. 4e-17;  
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 10  
 US-09-997-333-268  
 Sequence 268; Application US/0999733  
 ; GENERAL INFORMATION:  
 ; Patent No. 6953336  
 ; Sequence 268; Application US/0999733  
 ; GENERAL INFORMATION:  
 ; Patent No. 6953336  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sharman  
 ; APPLICANT: Gerber-Hanspetter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kjavian, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zemlin, Zemin  
 ; TITLE OF INVENTION: Sacred and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2710P1C27  
 ; CURRENT APPLICATION NUMBER: US/09/997,333  
 ; CURRENT FILING DATE: 2001-11-15  
 ; PRIORITY APPLICATION NUMBER: 60/049787  
 ; PRIORITY FILING DATE: 1997-06-16  
 ; PRIORITY APPLICATION NUMBER: 60/062250  
 ; PRIORITY FILING DATE: 1997-10-17

RESULT 9  
 US-99-796-158-2  
 ; Sequence 2, Application US/09796158  
 ; Patent No. 6939690  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; Deisher, Therese A.  
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0

PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075345  
PRIOR FILING DATE: 1998-02-15  
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PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088976  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091478  
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 ; PRIOR APPLICATION NUMBER: 60/091544  
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 ; PRIOR APPLICATION NUMBER: 60/091633  
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 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match Score 198, DB 2, Length 117;  
 Best Local Similarity 88.6%, Pred. No. 4e-17; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MPSPTVCSLLGMLWLDIAMGSSFSLSPHEHQVQVRPHKAP 44
Db	1	MPSPTVCSLLGMLWLDIAMGSSFSLSPHEHQVQQRKESKKP 44

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RESULT 11

US-09-992-598-268

Sequence 268, Application US/0992598

Patent No. 6956108

GENERAL INFORMATION:

- ; APPLICANT: Abhkenazi, Avi J.
- ; APPLICANT: Baker, Kevin P.
- ; APPLICANT: Botstein, David
- ; APPLICANT: Desnoyers, Luc
- ; APPLICANT: Eaton, Dan L.
- ; APPLICANT: Ferrara, Napoleone
- ; APPLICANT: Fong, Sherman
- ; APPLICANT: Gerber, Hanspeter
- ; APPLICANT: Geritsen, Mary E.
- ; APPLICANT: Goddard, Audrey
- ; APPLICANT: Godowski, Paul J.
- ; APPLICANT: Grimaldi, J. Christopher
- ; APPLICANT: Gurney, Austin L.
- ; APPLICANT: Klijavin, Ivar J.
- ; APPLICANT: Napier, Mary A.
- ; APPLICANT: Pan, James
- ; APPLICANT: Paoni, Nicholas F.
- ; APPLICANT: Roy, Margaret Ann
- ; APPLICANT: Stewart, Timothy A.
- ; APPLICANT: Tumas, Daniel
- ; APPLICANT: Watanaue, Colin K.
- ; APPLICANT: Williams, P. Mickey
- ; APPLICANT: Wood, William I.
- ; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P273OP1C20

CURRENT APPLICATION NUMBER: US/09/992,598

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/09787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/052250

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089532

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089538

PRIOR FILING DATE: 1998-06-17



RESULT 14  
US-09-252-991A-27248  
; Sequence 27248, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenstein et al.  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AEROCINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252, 991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074, 788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094, 190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 22248  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: *Pseudomonas aeruginosa*  
; US-09-252-991A-27248

Query Match 11.9%; Score 74; DB 2; Length 597;  
Best Local Similarity 27.4%; Pred. No. 2;  
Matches 34; Conservative 15; Mismatches 35; Indels 40; Gaps 6;  
Length: 597

Qy 3 SPGTIVCS-----LLIGLMLWDLAMAGS--SFLSPERQRVQVRP-PHIKAP 44  
Db 152 SPGPSSQGQDQAAPESIMMAMVLIGELLILLIGSIIALRQVGEVPEPR 211  
Qy 45 H-----VYPALPLPSNOLCDLEQQRHLMWSVSFQSTKDSGSDLTVSGRTWGLRVLNRLF 97  
Db 212 DSGRDMSVLEQLP---ELC-----FSQVIRBGGHAWVWAGQLOGLVVAIKAF 256  
Qy 98 PPSS 101  
Db 257 PPRS 260

Query Match 11.5%; Score 71.5; DB 2; Length 201;  
Best Local Similarity 27.6%; Pred. No. 0.89;  
Matches 32; Conservative 13; Mismatches 42; Indels 29; Gaps 6;  
Length: 201

Qy 10 LLIGLMLWDLAMAGSFLSPEIQRVQVRPHIKAPHHVVPALPLSNQLCDLEQQRHL 65  
Db 7 VLLVGVLGI-ASSIGA-----QEARRPPEHRSR-TPAWARQGVLLGVSAQDGLVVASQ 56  
Qy 66 -----WASVPSQSTKDSGSDLTVSGRTWGLRVLNRLFP-----PSSRERSRRSHQP 111  
Db 57 TKVOWQFTYQDRXDAFALLLEGSLSMGL-----AFPDAEKGPKQNAVRSFYQHSP 107

Search completed: December 21, 2005, 13:41:28  
Job time : 48 secs

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RESULT 15  
US-09-902-540-13645  
; Sequence 13645, Application US/09902540  
; Patent No. 6533447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and uses Thereof  
; FILE REFERENCE: 38-101158491B  
; CURRENT APPLICATION NUMBER: US/09/902, 540  
; CURRENT FILING DATE: 2001-07-10

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

- ① Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).
- ② Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: December 21, 2005, 13:32:53 ; Search time 12 Seconds  
(without alignments)  
69.538 Million cell updates/sec

Title: US-10-659-782B-32

Perfect score: 620

Sequence: 1 MNSPGTVCSLLLGMLWLDL.....PPSSRRRSRSHQPCSCPESPEL 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0<sup>\*</sup>

Listing First 45 summaries

Database : Published Applications AA New: \*

1: /cgn2\_6/protdata/2/pubpa/us08\_new\_pub.dep:\*

2: /cgn2\_6/protdata/2/pubpa/us05\_new\_pub.dep:\*

3: /cgn2\_6/protdata/2/pubpa/us07\_new\_pub.dep:\*

4: /cgn2\_6/protdata/2/pubpa/pct\_new\_pub.dep:\*

5: /cgn2\_6/protdata/2/pubpa/us09\_new\_pub.dep:\*

6: /cgn2\_6/protdata/2/pubpa/us10\_new\_pub.dep:\*

7: /cgn2\_6/protdata/2/pubpa/us11\_new\_pub.dep:\*

8: /cgn2\_6/protdata/2/pubpa/us60\_new\_pub.dep:\*

<sup>\*</sup>red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	198	31.9	117	US-10-131-B26A-442 Sequence 442, App
2	66	10.6	258	US-10-131-B24-1368 Sequence 1368, App
3	63	10.2	303	US-11-186-224-193 Sequence 193, App
4	63	10.2	903	US-10-189-742-142 Sequence 142, App
5	61.5	9.9	1613	US-11-108-528-84 Sequence 84, App
6	61	9.8	96	US-11-000-46-931 Sequence 931, App
7	61	9.8	260	US-11-182-946-8 Sequence 8, App
8	59.5	9.6	465	US-10-973-528-164 Sequence 164, App
9	59.5	9.6	1615	US-11-108-528-80 Sequence 80, App
10	58.5	9.4	1613	US-11-108-528-86 Sequence 86, App
11	58	9.4	255	US-11-147-047-36 Sequence 36, App
12	58	9.4	1627	US-10-921-224-1283 Sequence 1283, App
13	57.5	9.3	500	US-11-087-100-30 Sequence 30, App
14	57.5	9.3	500	US-11-087-084-30 Sequence 30, App
15	57.5	9.3	500	US-11-087-085-30 Sequence 30, App
16	57.5	9.3	808	US-11-110-082-38 Sequence 38, App
17	57.5	9.3	1503	US-11-087-100-6 Sequence 6, App
18	57.5	9.3	1503	US-11-087-084-6 Sequence 6, App
19	57.5	9.3	1503	US-11-087-085-6 Sequence 6, App
20	57.5	9.3	1798	US-11-080-991-96 Sequence 96, App
21	57.5	9.3	2061	US-11-077-386-27 Sequence 27, App
22	57	9.2	980	US-11-064-246-10 Sequence 10, App
23	57	9.2	1162	US-10-451-375-3 Sequence 3, App
24	57	9.2	1198	US-10-451-375-4 Sequence 4, App
25	57	9.2	4655	US-10-995-561-556 Sequence 556, App

## ALIGNMENTS

RESULT 1  
US-10-131-B26A-442  
; Sequence 442, Application US/10131826A  
; Publication No. US20030245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Destroyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel K.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131-826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; Remaining Prior Application data removed - See File Wrapper or PALM.



APPLICANT: Marvin, Martha  
 APPLICANT: Li, Dean Y.  
 APPLICANT: Wang, Elizabeth  
 APPLICANT: Chen, C. M. Amy  
 APPLICANT: Shamah, Steven M.  
 TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL  
 TITLE OF INVENTION: PROLIFERATION  
 FILE REFERENCE: HYDR-P01-041  
 CURRENT APPLICATION NUMBER: US/11/108,528  
 CURRENT FILING DATE: 2005-04-18  
 PRIOR APPLICATION NUMBER: US 60/563,137  
 PRIOR FILING DATE: 2004-04-16  
 PRIOR APPLICATION NUMBER: US 60/598,368  
 PRIOR FILING DATE: 2004-08-02  
 NUMBER OF SEQ ID NOS: 86  
 SEQ ID NO: 84  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 LENGTH: 1613  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-108-528-84

RESULT<sup>6</sup>  
 Query Match 9.9%; Score 61.5; DB 7; Length 1613;  
 Best Local Similarity 27.9%; Pred. No. 43;  
 Matches 34; Conservative 10; Mismatches 49; Indels 29; Gaps 7;

Qy 2 PSPGTVCSLLIGMMLWDLAMAGSSFLSPS--GYSSNSPETHRSYRPSYRHFAP--PHKAPHVVPALPQNLC 57  
 Db 1489 PSPATERSHYNMEF-----  
 Qy 58 DLEQQRHLWASVFSQSTKDSGSDDLTVSGRTGLRVNRLFPSSRERSR---RSHQPSR 113  
 Db 1538 D-----SPYAPSRRT-SVATARGTSDLNAYSEPPPTERSQYIUSAENYESC 1587

Qy 114 SP 115  
 Db 1588 PP 1589

RESULT<sup>6</sup>  
 US-11-000-463-931  
 Sequence 931, Application US/11/000463  
 Publication No. US2005026642A1

GENERAL INFORMATION:  
 APPLICANT: Tang, Y Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Qian, Xiaochong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Drmanic, Radivoje T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785CIP4CN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 931  
 LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-931

Query Match 9.8%; Score 61; DB 7; Length 96;  
 Best Local Similarity 26.3%; Pred. No. 17;  
 Matches 20; Conservative 7; Mismatches 21; Indels 28; Gaps 3;

Qy 41 HKAPHVVPALPPLNSQCDLQQRRHLWASVFSQSTKDSGSDDLTVSGRTGLRVNRLFPSSRERSR---EAEGRSGSDF-----WDGGCLGRVTPPS 100  
 Db 46 HCSRHTVQVSPSSST-----  
 Qy 101 SRERSRSHQPSCSPE 116  
 Db 85 -----IHVTSCSAE 93

RESULT<sup>7</sup>  
 US-11-182-946-8  
 Sequence, Application US/11182946  
 Publication No. US2005025510A1  
 GENERAL INFORMATION:  
 APPLICANT: Wei, Ying-Fei  
 APPLICANT: Ni, Jian  
 APPLICANT: Gentz, Reiner  
 APPLICANT: Ruber, Steven  
 TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
 FILE REFERENCE: 1488 1280004  
 CURRENT APPLICATION NUMBER: US/11/182,946  
 CURRENT FILING DATE: 2005-07-18  
 PRIOR APPLICATION NUMBER: US/10/186,643  
 PRIOR FILING DATE: 2002-07-02  
 PRIOR APPLICATION NUMBER: US/09/573,986  
 PRIOR FILING DATE: 2000-05-18  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 8  
 LENGTH: 260  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-182-946-8

Query Match 9.8%; Score 61; DB 7; Length 260;  
 Best Local Similarity 20.8%; Pred. No. 5.5;  
 Matches 25; Conservative 17; Mismatches 34; Indels 8  
 Gaps 4;

Qy 2 PSPGTCS-----LILLGMLWLAMAGSSFLSPHQRYQVRPPHKAPHVVPALPQN 55  
 Db 179 PPQRSLSCSSDFTRILVIFSGMFLVFTLAGFL---HORRYRSNKGESPYPBEPGR-- 233  
 Qy 56 LCDLBOORHLWASVFSQSTKDSGSDDLTVSGRTGLRVNRLFPSSRERSRSHQPSCSPE 115  
 Db 234 -----YSCPREEEGSTPI-----  
 RESULT<sup>8</sup>  
 US-10-873-528-164  
 Sequence 164, Application US/10873528  
 Publication No. US2005027681A1  
 GENERAL INFORMATION:  
 APPLICANT: Microbial Technics Limited  
 APPLICANT: Gilbert, Christophe FG  
 APPLICANT: Hansbro, Phillip M  
 TITLE OF INVENTION: Proteins  
 FILE REFERENCE: PNC/P21129NO  
 CURRENT APPLICATION NUMBER: US/10/873,528  
 CURRENT FILING DATE: 2004-06-23  
 PRIOR APPLICATION NUMBER: US/09/769,787  
 PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: GB 9816337.1  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: US 60/125164  
 PRIOR FILING DATE: 1999-03-19  
 NUMBER OF SEQ ID NOS: 388  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 164  
 LENGTH: 465  
 TYPE: PRT  
 ORGANISM: *Streptococcus pneumoniae*  
 US-10-873-528-164

Query Match 9.6%; Score 59.5; DB 6; Length 465;  
 Best Local Similarity 24.7%; Pred. No. 16;  
 Matches 23; Conservative 13; Mismatches 38; Indels 19; Gaps 2;

Qy 13 LGMLWILDAMAGSSFLSPHORVQVRPHAKPHVYPALPISNQLCDLEQQRHLWASVFSQ 72  
 Db 11 LGTVVVLSAFTVANSVAQEETETSEVTPKLVQVAPPTPSE-----vQ 54

Qy 73 STKDGSGLTVSGRTWGLRVLNRLFPPSSRSERS 105  
 Db 55 PTSDNSSEVTVQPRTVBTTVYKD--PSSTATET 84

RESULT 9  
 US-11-108-528-80  
 Sequence 80, Application US/11108528  
 Publication No. US20050261189A1  
 GENERAL INFORMATION:  
 PRIOR: Larsen, Glenn  
 APPLICANT: Marvin, Martha  
 APPLICANT: Li, Dean Y.  
 APPLICANT: Wang, Elizabeth  
 APPLICANT: Chen, C. M.  
 APPLICANT: Steven M.  
 TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL  
 FILE REFERENCE: HYDR-P01-041  
 CURRENT APPLICATION NUMBER: US/11/108,528  
 CURRENT FILING DATE: 2005-04-18  
 PRIOR APPLICATION NUMBER: US 60/563,137  
 PRIOR FILING DATE: 2004-04-16  
 PRIOR APPLICATION NUMBER: US 60/598,368  
 PRIOR FILING DATE: 2004-08-02  
 NUMBER OF SEQ ID NOS: 86  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 36  
 LENGTH: 465  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-108-528-80

Query Match 9.6%; Score 59.5; DB 7; Length 1615;  
 Best Local Similarity 25.0%; Pred. No. 72;  
 Matches 30; Conservative 14; Mismatches 41; Indels 35; Gaps 7;

Qy 2 PSPGTVCSLLIGMLWILDAMAGSSFLSPHORVQVRPHAKPHV-----PAIPLSNQL 56  
 Db 1502 PSPATDPSLYNMDFY-----SSNIP-----ATVRP-----YRPYTRGMAPPITPCSTDV 1547  
 Qy 57 CDLBQQRHLWASVFSOSTKDGSDLTSGSLTVSGRTWGLRVLNRLFPPSSRSERS-RSHOPSCSP 115  
 Db 1548 CDSYSASRMKA--SKYLLDLSND-----SDYPPPPTPHSSQYLSAEDSCCPP 1592

RESULT 10  
 US-11-108-528-86  
 Sequence 86, Application US/11108528  
 Publication No. US20050261189A1  
 GENERAL INFORMATION:  
 PRIOR: Larsen, Glenn  
 APPLICANT: Marvin, Martha

Query Match 9.4%; Score 58; DB 7; Length 255;  
 SEQ ID NO 36  
 LENGTH: 255  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-147-047-36

Query Match 9.4%; Score 58.5; DB 7; Length 1613;  
 Best Local Similarity 27.0%; Pred. No. 94;  
 Matches 33; Conservative 11; Mismatches 49; Indels 29; Gaps 7;

Qy 2 PSPGTVCSLLIGMLWILDAMAGSSFLSPHORVQVRP-----PHKAPHVYPALPLSNQLC 57  
 Db 1489 PSPATERSHYTMEEF-----GYNSNSPSTHRSYRPSYRHFAP-----PTTCSTDVC 1537  
 Qy 58 DLEQQRHLWASVFSOSTKDGSDLTSGSLTVSGRTWGLRVLNRLFPPSSRSERS-RSHOPSC 113  
 Db 1538 D-----SDYAPSRRMT-SVATAKGTSVDNYDSEPVPPPTRSQYLSAENYESC 1587

Query Match 9.4%; Score 58.5; DB 7; Length 1613;  
 Best Local Similarity 27.0%; Pred. No. 94;  
 Matches 33; Conservative 11; Mismatches 49; Indels 29; Gaps 7;

Qy 2 PSPGTVCSLLIGMLWILDAMAGSSFLSPHORVQVRP-----PHKAPHVYPALPLSNQLC 57  
 Db 1489 PSPATERSHYTMEEF-----GYNSNSPSTHRSYRPSYRHFAP-----PTTCSTDVC 1537  
 Qy 58 DLEQQRHLWASVFSOSTKDGSDLTSGSLTVSGRTWGLRVLNRLFPPSSRSERS-RSHOPSC 113  
 Db 1538 D-----SDYAPSRRMT-SVATAKGTSVDNYDSEPVPPPTRSQYLSAENYESC 1587

RESULT 11  
 US-11-147-047-36  
 Sequence 36, Application US/11147047  
 Publication No. US2005026068A1  
 GENERAL INFORMATION:  
 PRIOR: Agarwal, Pankey  
 APPLICANT: Agarwal, Pankey  
 APPLICANT: Murdock, Paul R.  
 APPLICANT: Rizvi, Safia K.  
 APPLICANT: Smith, Randall F.  
 APPLICANT: Xiang, Zhaoying  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 FILE REFERENCE: GPS50016  
 CURRENT APPLICATION NUMBER: US/11/147,047  
 CURRENT FILING DATE: 2005-06-07  
 PRIOR APPLICATION NUMBER: US/10/221,097  
 PRIOR FILING DATE: 2002-09-06  
 PRIOR APPLICATION NUMBER: PCT/US01/07143  
 PRIOR FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 60/187,107  
 PRIOR FILING DATE: 2000-03-06  
 PRIOR APPLICATION NUMBER: 60/236,874  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/188,916  
 PRIOR FILING DATE: 2000-03-13  
 PRIOR APPLICATION NUMBER: 60/237,846  
 PRIOR FILING DATE: 2000-10-03  
 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 36  
 LENGTH: 255  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-147-047-36

Best Local Similarity 20.5%; Pred. No. 12; Mismatches 42; Indels 60; Gaps 6;  
 Matches 30; Conservative 14; Software: Patentin version 3.3  
 SEQ ID NO: 30 LENGTH: 500

PRIOR FILING DATE: 2001-04-16  
 PRIORITY NUMBER: 60/298,796  
 PRIORITY FILING DATE: 2001-05-15  
 PRIORITY APPLICATION NUMBER: 60/323,269  
 PRIORITY FILING DATE: 2001-09-18  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: Patentin version 3.3

Qy 5 GTVCSLLLGMWLDLA---MAGSSFLSPHEHQYQVRPP----- 40  
 Db 23 GHICGSSLIAPISWLSSAAHCFMTGRCPTRRTRRSALTRKRRRAYNHSQGSDLALL 82  
 Qy 41 ---HKAPHVVPALPLSNOLQDLEQQBH-----LWASVSQSTKDGSQDLTVSG--RTW 88  
 Db 83 QLAQHPTHTPLCLP-----QPAHFRPGASCHATGWINDQTSDAPSLSLSPAPSTLRN 133  
 Qy 89 GLRVLNRLFPPSRERSRSRSHQPSCS 114  
 Db 134 RLRLISR-----PTCN 144

Query Match 9.3%; Score 57.5%; DB 7; Length 500;  
 Best Local Similarity 25.3%; Pred. No. 30;  
 Matches 25; Conservative 4; Mismatches 41; Indel 8 29; Gaps 4;

Qy 17 WLDLAMAGSSFLSPHEHQYQVRPPH-----KAPHVVPALPLSNOLQDLEQQHLW---- 66  
 Db 395 WEDSYMPGSLGVESMFOVLEAIAAHEDLAGRKARHCCP-----HLCARPRARSNSYRQG 448

Qy 67 -----ASVFSQSTKDGSQDLTVSGRTW--GLRV 92  
 Db 449 LTPKSKKMDSEVHIVSVDAHDGVVDDLVADGFLWADSLRV 487

---

RESULT 14  
 US-11-087-1234-1283  
 Sequence 1283, Application US/10821234  
 Publication No. US2005025514A1  
 GENERAL INFORMATION:  
 APPLICANT: Labat, Ivan  
 APPLICANT: Stache-Crain, Birgit  
 APPLICANT: Andarmani, Susan  
 APPLICANT: Tang, Y. Tom  
 FILE REFERENCE: Methods for Diagnosis and Treatment of Preeclampsia  
 CURRENT APPLICATION NUMBER: US/10/821,234  
 CURRENT FILING DATE: 2004-04-07  
 PRIOR APPLICATION NUMBER: US 60/462,047  
 PRIOR FILING DATE: 2003-04-07  
 SEQ ID NO: 1704  
 SOFTWARE: PT SEQ\_Genes Version 1.0  
 SEQ ID NO: 1283  
 LENGTH: 1627  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-821-1283

Query Match 9.4%; Score 58; DB 6; Length 1627;  
 Best Local Similarity 23.8%; Pred. No. 1.1e+02;  
 Matches 29; Conservative 11; Mismatches 46; Indels 36; Gaps 4;

Qy 5 GTVCSLLLGMWLDLAMAGSSFL-----SPEHQYQVRPPHKA- 43  
 Db 707 GSACHCLEGRILIVQYASNAASSPMPCPSGPWSPREALEGHPDVEQPKTSYRTWSNSAV 766  
 Qy 44 -PHVVPALPLSNOLQDLE-----QQRHLWASVSQSTKDGSQD-----LTIVSGRTW 88  
 Db 767 NPHTVPPACPEPGCYCLEFLYPLVPESTLIVWTFWSTNDSSGAVNDKILAVSGKNI 826  
 Qy 89 GL 90  
 Db 827 SL 828

Query Match 9.3%; Score 57.5%; DB 7; Length 500;  
 Best Local Similarity 25.3%; Pred. No. 30;  
 Matches 25; Conservative 4; Mismatches 41; Indel 8 29; Gaps 4;

Qy 17 WLDLAMAGSSFLSPHEHQYQVRPPH-----KAPHVVPALPLSNOLQDLEQQHLW---- 66  
 Db 395 WEDSYMPGSLGVESMFOVLEAIAAHEDLAGRKARHCCP-----HLCARPRARSNSYRQG 448

Qy 67 -----ASVFSQSTKDGSQDLTVSGRTW--GLRV 92  
 Db 449 LTPKSKKMDSEVHIVSVDAHDGVVDDLVADGFLWADSLRV 487

---

RESULT 15  
 US-11-087-085-30  
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 Publication No. US20050266440A1  
 GENERAL INFORMATION:  
 APPLICANT: Metz, James  
 APPLICANT: Barclay, William  
 APPLICANT: Flatt, Jerry  
 APPLICANT: Kuner, Jerry  
 TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase  
 FILE REFERENCE: 2997-19  
 CURRENT APPLICATION NUMBER: US/11/087,084  
 CURRENT FILING DATE: 2005-03-21  
 PRIOR APPLICATION NUMBER: 09/231,899  
 PRIOR FILING DATE: 1999-01-14  
 PRIOR APPLICATION NUMBER: 60/284,066  
 PRIOR FILING DATE: 2001-04-16  
 PRIOR APPLICATION NUMBER: 60/298,796  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/323,269  
 PRIOR FILING DATE: 2001-09-18  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: Patentin version 3.3  
 SEQ ID NO: 30 LENGTH: 500  
 TYPE: PRT  
 ORGANISM: Schizochytrium sp.  
 US-11-087-084-30

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 ; APPLICANT: Metz, James  
 ; APPLICANT: Barclay, William  
 ; APPLICANT: Flatt, James  
 ; APPLICANT: Kuner, Jerry  
 ; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase System and Uses Thereof  
 ; FILE REFERENCE: 2997-29  
 ; CURRENT APPLICATION NUMBER: US11/087,085  
 ; CURRENT FILING DATE: 2005-03-21  
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Qry      Query Match 9 3%; Score 57.5; DB 7; Length 500;  
 Best Local Similarity 25.3%; Pred. No. 30;  
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Qry      67 -----ASVFQSQTIDSGSDLTVSERTW--GLRV 92  
 Db      449 LTPKSKKMDSVHIVSYDAHDGVVDLVADGFLWDSLKV 487

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